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b_sts1:

em_sy:* em_un:* em_v1:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                       1344157 seqs, 7733874588 residues
                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                             US-09-105-117I-1_COPY_1421_2293
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Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
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X96471 C. glutamicu A93933 Sequence 2 AL337613 Streptomy U34849 Mycobacteri 186263 Sequence 17 Z74025 Mycobacteri AB011413 Streptomy

AX063767 Sequence

AX063767 CGLYSEG A93933 SC5F8 MBU34849

186263 MTCY39 AB011413

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X73026 E.coli gene
M62865 E.coli chro
X66836 E.coli serA
AE000375 Escherich
AE005521 Escherich
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AE004639 Pseudomon
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AY017305 Synechoco
A3817 P.putida ca
AL008883 Mycobacte
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AL162755 Neisseria
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56 Escherich
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BASF AKTIENGESELEGHAFT (DE)
Location/Qualifiers
e 1. .993
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ACO20850_0
ACO208577
ACO02563
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Corynebacterium glutamicum
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SSVEQLDNSLDSLNNLEFSDAELEAIDEISHDAGINIWARATDSKTREN"
                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (07-MAR-1996) M.M. Vrljic, Institut fuer Biotechnologie
1, Forschungszentrum Juelich, Postfach 1913, D-52425 Juelich, FRG
Location/Qualifiers
                                                                                                                                                                                                                        of cellular function;
                                                                             lysE gene; lysG gene; Lysine export regulator protein; exporter protein; Lysine governor. Corynebacterium glutamicum. Corynebacterium glutamicum Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                           Actinomycetales; Corynebacterineae; Corynebacteriaceae;
Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulator protein"
                                                                                                                                                                                                    Vrljtc,M., Sahm,H. and Eggeling,L.
A new type of transporter with a new type of cel
L-lysine export from Corynebacterium glutamicum
Mol. wicrobiol. 22 (5), 815-826 (1996)
97126810
                                                                                                                                                                                                                                                                                                                                                                               1. .2374
/organism="Corynebacterium glutamicum"
                  BCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Lysine exporter protein"
/protein_id="CAA65324.2"
/db_xref="G1:13397387"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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/db_xref="G1:1729756"
/db_xref="SPTREMBL:P94634"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"Lysine export r
/protein_id="CAA65323.1"
/db_xref="GI:1729754"
                                  genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Lysine governor"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1723. .2352)
/gene="orf3"
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                                                                                                                                                                                                                                                                                                                                                                                                           /strain="R127"
/db_xref="taxon:1718"
complement(82. .954)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="lysg"
complement(82. ,954)
                bp DNA
and lysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
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/transl_table=11
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/gene="lysE"
1025. .1726
/gene="lysE"
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                                                                                                                                                                                                                                                                              2 (bases 1 to 2374)
Vrljic, M.M.
                                                               GI:1729753
                                                                                                                                                                                         (bases 1 to 2374)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="lysG
                  2374 |
1ysE
                             C.glutamicum 1
X96471
X96471.1 GI:1
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355

099 295 720 235 780 175

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Stradud.

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Kroph et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the EramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-JUN 2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALISTOGIS.1 GI:8347023
amino acid decarboxylase; anti-sigma factor; integral membrane protein; LuxR-family regulator; LySR-family transcriptional regulator; membrane transport protein; oxidoreductase; regulatory protein; RNA polymerase sigma factor; serine/threonine protein kinase; stress-inducible protein; TetR-family transcriptional regulator; thioredoxin reductase; threonine dehydratase; two-component sensor histidine kinase.
Streptomyces coelicolor A3(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinomycetales, Streptomycineae, Streptomycetaceae, Streptomyces. 1 (bases 1 to 33285)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), 01 (first CDS), c (complementary strand).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
09-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (bases 1 to 33285)
Thomson, N.R., Parkhill, J., Barrell, B.G. and Rajandream, M.A. Direct Submission
                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCT
                                                                                                                                                                                                                                         841 gttgatgcagcaatcgagggattgcggccttag 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                SC5F8 33285 bp DNA Streptomyces coelicolor cosmid 5F8.
                                                                                                                                                                                                                                                                                                 114 GTTGATGCAGCAATCGAGGGATTGCGGCCTTAG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 33285)
Seeger, K.J. and Harris, D.
Unpublished
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SC5F8/c
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/joce="SC5F8.03c, unknown, len: 225 aa. Similar to several proteins of undefined function including: Deinococcus radiodurans TR:09RwP1(EMBL:AB001920) conserved hypotheitaal protein (254 aa), fasta scores opt: 467 z-score: 555.6 E(): 1.8e-23 36.6% identity in 205 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="wkgdlessehmyoparapcmtvenskciryavngemlarogami
ayrgnloferkgogovggmlkravtgeglplmavrgogeawfaneaoncfvvevepedde
ftvngrnvlcfdaslsyrlatvkgsgiaggglfnsvftgogrlglvcegnplvIpvso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="SCFFB.04c, unknown, len: 434 aa. Similar to
Streptomyces coelicolor TR:09X0W9(EMBL:AL096743) putative
transport associated protein, SCI7.21 (399 aa), fasta
scores opt: 428 z-score: 449.2 E(): 1.5e-17 38.3% identity
in 209 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTHAGWACVTGGPSGDTYWTALWAVPLTPDGLARTTAEVVGLTNRERAGAGLPALAVD
ARLTAAAQAHSADMVTRDFYSHTDPDGGKPWDRAAAAGADRRSVGENIACGQRSPAEV
VEGWMNSPGHRANILEAGFTHIGVGLAGGGRAGTYWTQLLGG"
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//gene="SCSF8.05c"
complement(3562. .6528)
//gene="SCSF8.05c"
//gene="SCSF8.05c"
//gene="SCSF8.05c"
//fore="SCSF8.05c"
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RrQ9Xn4(EMBL:AL079355) SC4C6.06 (893 aa), fasta scores opt: 305 z-score: 328.7 E(): 7.7e-11 26.48 identity in 910 aa overlap and TR:Q9Z573(EMBL:AL035569) SC8D9.18 (1091 aa), fasta scores opt: 857 z-score: 926.1 E(): 0 36.58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identity in 1077 as overlap. Contains a Prosite hit to PS00017 ATP/GTP-binding site motif A (P-loop) Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLLRFLLGRGVLQRPAGGAPGHRLALFASYRADDLHRRHPLRPLLAELVRLPGVERLE
LRPLPDSDVARLVRLLRERRLPDSTVRRIVERAEGNAFYAEELVAATDAPAGGVPSGL
ADVLLIRFEQLSETAQQVLRTAAVAGRRVGHDLLRDAVGLPEEELESALREAVERQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QYPVHVDTDAVVGWSAGLATSLHRSQSIGSMLRGGSGEAVQLVLQGEGFVVVRPSEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mSDLVPGGNVPLPGGPVSVRVPGGFDVSALVTDEGGKVGGDADF
VFYNQPEAPGARLRDDTLTVDPARLRRGAARVTVAVGPSDPGTPLGALPSPTVLVTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGRTVARFTPARPGRETVLLLVEFYRRGEGWKVRALGQGYADGLAGLARDFGVEVTDD
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GVGKTRTLHEAAGRAAAAGTTVLTGHCVDLGDVGLPYLPFTEILGVLAADERFAAVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHPVADRLLGGGPDDGTDAAPSRLRLFEGVAALLTELADVAPLLLVLEDLHWADQSSR
                                                                                                                                                                                                                                                                                                                          overlap and Straptomyces coelicolor
TR:CAB70638(EMBL:AL137242) SC8F4.12C (239 aa), fast
scores opt: 397 z-score: 474.2 E(): 6.1e-19 36.1%
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Pred. No. 6.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein SCSFB.03c."
/protein_id="CAB93731.1"
/db_xref="G1:8347026"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein SC5F8.04c."
/protein_id="CAB93732.1"
/db_xref="GI:8347027"
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                                                                                                                                                                                                                                                                                                                                                                                                                                identity in 183 aa overlap."
/codon.start=1
/transl_table=11
                                              complement(1477. .2154)
/gene="SC5F8.03c"
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complemen+/21/
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/gene="SC5F8.04c"
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                                                                                                                                                                                                                                                                                                                                                                                                               scores opt:
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50.9%;
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Best Local Similarity
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//gene="SCSFB.02c"
//gene="S
ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase, partials CDS, len:> 114 aa. Similar to many proposed Streptomyces coelicolor serine/threonine protein kinases e.g. TR:CABB2014 (EMBL:AL161755) SCD63.07 (717 aa), fasta scores opt: 172 z-score: 222.0 E(): 6.8e-05 33.0% identity in 103 aa overlap. Overlaps and extends into CDS SCBH.01 on the adjoining cosmid."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARSVEIAEEBGALVRLTDGMDSAFALVTRLREEGLTLVHPFDDPVVVAGQGTVGLEF
BEABSULTOVLVSIGGGGLIAGVAAALBALRPGVRWWEVETSCABAMSRALAAGGPLT
VPLSSVYTTLSAPSVSRLTYDHVAELVTEVLVVPDRRAVRGSIALAEHAKVWTEPAAG
CLLPAARRVVERVGDGARIGLVVCGGNATVGDMAVWADRFGLR
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QRTGSFKARGATAKLLSLTEAERAAGVVAVSGGNHGIAVAVMAAALDVKATVVMPRTA
                                                                                                                                                         sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid 5F8 lies on genomic restriction fragment Asel-A bordered by cosmids 5H1 and 4G10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1. .108)
/gene="SC5F8.01c"
/note="nominal overlap with cosmid SC5H1 between bases
                                                                                                                       IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="SC5F8.01c, possible serine/threonine protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="fam match to entry PF00291 S_T_dehydratase,
Pyridoxal-phosphate dependent enzyme, score 210.10,
E-value 3.3e-59"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative serine/threonine protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"PS00165 Serine/threonine dehydratases
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                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1.33285
/organism="Streptomyces coelicolor A3(2)"
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complement(1477. .2154)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="A3(2)"
/db_xref="taxon:100226"
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/gene="SC5F8.02c"
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/gene="SC5F8.02c"
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/gene="SC5F8.01c"
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complement
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Actinobacteria; Actinobacteridae;

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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 10567 to 11392)
Oettinger, T. and Andersen, A.B.
Cloning and B-cell-epitope mapping of MPT64 from Mycobacterium tuberculosis H37Rv
                                                                                                                                                                                                                                                            Mahalras,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stoves
Direct Submission
Submitted (24-AUG-1995) Mark J. Hickey, Molecular Micro.,
PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119,
Location/Qualifiers
                                                                                                                                            Mahairas, G.G., Sabo, P.J., Hickey, M.J., Singh, D.C., Molecular analysis of genetic differences between boxis BCG and virulent M. bovis.
J. Bacteriol. 178 (5), 1274-1282 (1996)
                                                                                                            Infect. Immun. 62 (5), 2058-2064 (1994) 94222581
   Bacteria; Firmicutes;
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                                                                                                                                                                                                                               193 caagcagcgcggaaaatggtgttgctgcaagcagaaactaaagcgcaactatctggacgc 252
 Gaps,
                                  72
                              caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc
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 15;
 Mismatches 414; Indels
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Conservative
Matches 444;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          gccttgctgaa....atcccgttaaccatcgccatcaacgcagattcgctatccacatgg 306
                                                                                                                                                   Gaps
13652. .13675
/note="one of two imperfect direct repeats located
near the deletion breakpoints"
1 4682 c 4603 g 2759 t
                                                                                                                                                                                ctttccatttccccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt
                                                                                                                                                                                                                                                                            CTACATGTCACCCCTCGGCTGTCAGTCAGCGCATCAAGTCGTTGGAGCAGCAGGTCGGC
                                                                                                                                                                                                                                                                                                                                          4979 caggiccigergacaeggaaaagccargreegcgacgacgcaggiarcccgcrerre
                                                                                                                                                                                                                                                                                                                                                                                                          cgagtgttggtatcgcgcacccaaccggccaagcaaccgaagcgggtgaagtccttgtg
                                                                                                                                                 18;
                                                                                                                   Length 14844;
                                                                                                                                                   Indels
                                                                                                                                 Pred. No. 8.4e-24;
0; Mismatches 409;
                                                                                                                   DB 3;
                                                                                                              Score 122.6;
Pred. No. 8.4
                                                                                                                   14.0%;
49.9%;
                                                                                                                                                   426; Conservative
                                                                                                                   Query Match
Best Local Similarity
                                                    2800
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immunogenic protein (mpt64)

27-APR-1996

BCT

MBU34849 14844 bp DNA Mycobacterium bovis deletion region 2,

U34849.1 GI:1049224 Mycobacterium bovis. Mycobacterium bovis

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

gene, complete cds. U34849

DEFINITION

/translation="mrikifmlutavvllccsgvataapktyceelkgtdtggacqig msdpaxninislpsyypdgkslenyiaqtrdkflsaatsstpreapyelnitsatygs aipprgtgavvlkvyqnaggthptttykafdmdgayrkpitydtlmgadtdplvvfp IVQGELSKQTGQQVSIAPNAGLDPVNYQNFAVTNDGVIFFFNPGELLPEAAGPTQVLV

PRSAIDSMLA"

/protein_id="AAC44034.1" /db_xref="GI:1049225"

protein"

/gene="mpt64" /note="immunogenic /transl_table=11 /product="MPT64" /codon_start=1

10705. 11391

or

at

1. 14844

/Organism="Mycobacterium bovis"

/db_xref="taxon:1765"

2864. 2888

/note="one of two imperfect direct repeats located at or near the deletion breakpoints"

/note="this interval is completely absent in the closely note="this uterval is completely absent in the closely related, but avirulent strain Mycobacterium bovis BCG"

/gene="mpt64"

and Stover, C.K.

(bases 1 to 14844)

USA

Stover, C.K.

and

Mycobacterium

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Mycobacterium tuberculosis H37Rv complete genome; segment 89/162. 274025 AL123456 Z74025.1 GI:3261586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5553 TTTTCGGCCGTGTTCGACG-----GTCTCGGCGACGTCCTGCTCGACGTTCGGATC 5603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6024 TATTGGCAATGCTGGAAACTGGACAGTCCGATCATCGCGCGAATTACCGACACGGTGAGG 6083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tttggtgaggcaattcgccgaggccttggttggggacttcttcccgaaacccaagctgct 723
                                                                                                                                                                                                                                                                                                                                                   tttcctcccgtgttcaacgaggtagcttcttggggttggagcaacgctcacgctgcgcttg 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cccatgctaaaagcaggagaagtgatcctcctcgatgagatacccattgacacaccgatg 783
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1 (bases 1 to 38500)

1 (bases 1, Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cg---cgtcgatggtcctgtgggggggggggggtatccattgtcccgtcggcggaaggt
                     5493 GCGTCGCTGAAACGCACCGGATCACCATTGCGGTAAACGCCGATTCCATGGCGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cgagtgttggtatcgcgcacccaaccggccaaagcaaccgaagcgggtgaagtccttgtg
                                                                                                                                          CAGGTGCTGGTCAGGGAAAAGCCATGTCGGGCGACGACGCAGGTATCCCGCTGTTG
                                                                                                                                                                                     caagcagcgcggaaaatggtgttgctgcaagcagaaactaaagcgcaactatctgg--ac
                                                                                                                                                                                                                                                                     gccttgctgaa----atcccgttaaccatcgccatcaacgcagattcgctatccacatgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGGACCAGGACCATTCCGCGGGCTGCTACGGGAGGGTGTGGCGATGGGCGCGGGTGACC
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Stover, C. Kendall and Mahairas, G.G.
Virulence-attenuating genetic deletions deleted from mycobacterium
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                                                                                                   TTTTCGCCCGTGTTCCACG-----GTCTCGCCGACGTCCTGCTCGACGTTCGGATC 5209
                                                                                                                                                                                                                                                                 5270 acceaecegaaccegerecegerecegerecegerececeregereaarececracera 5329
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                                                                                                                                            gaagatgaagcgcacacattatccttgctgcggcgtggagatgttttaggagcggtaacc 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tttggtgaggcaattcgccgaggccttggttggggacttcttcccgaaacccaagctgct 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ttcctcccgtgttcaacgaggtagcttcttgggggtggagcaacgctcacgctgcgcttg
                                                                                                                                                                      cgtgaagctaatcccgtggcgggatgtgaagtagtagaacttggaaccatgcgccacttg
                                                                                                                                                                                                                                                                                                              gccattgcaacccctcattgcgggatgcctacatggttgatgggaaactagattgggct
                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGGCTAAAAGCTCCGTCACTGGCGTGGAATCGTGACGATGGGGCTGCAGGACATGTTGGTG
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Pred. No. 8.4e-24;
0; Mismatches 409;
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186263
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a 4791 c 4729 g
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Best Local Similarity 49.9%;
Matches 426; Conservative
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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE

5843

909

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MEDLINE REMARK

JOURNAL

TITLE

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COMMENT

REFERENCE

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/product="Pp_pers"
/protein_id="CaA98400.1"
/db_xref="G1:1d0472"
/db_xre
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/gene="Rv1982c"
/note="Rv1982c, (MTCY39.37), len: 139. Similar to
Mycobacterium tuberculosis 292772|MTY20H10_5 (131 aa)
FASTA scores: opt: 288 z-score: 388.5 E(): 4.1e-14; 40.28
identityin 127 aa overlap, also similar to Rv2759c, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MIVDTSAVVALVQGERPHATLVAAALAGAHSPVMSAPTVAECLI
VLTARHGPVARTIFERLRSEIGLSVSSFTAEHAAATQRAFLRYGKGRHRAALNFGDCM
TXATAQLGHQPLLAVGNDFPQTDLEFRGVVGYWPGVA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MTGKLVERVHAINWNRLLDAKDLQVWERLTGNFWLPEKIPLSND
LASWQTLSSTEQQTTIRVFTGLTLLDTAQATVGAVAMIDDAVTPHEEAVLTNWAFMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHAKSYSSIFSTLCSTKQIDDAFDWSEQNPYLQRKAQIIVDYYRGDDALKRKASSVML
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ADHREYTCELLHTLYANEIDYAHDLYDELGWTDDVLPYMRYNANKALANLGYQPAFDR
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YYIFATYTTYVDFGNGIVTAPTANVNVLLSIPPTSPALSTFYESALLADPTTPTERAYF
GAVGDGVLGVGPANAPGESIPTMALPGDLNGGVLIDAPAGELVFGPNPLPAPNVEV
VGSPTTTLYVKIDGGPPIPVPSIIDSGGVPGTIPSYVIGSGTLBANTNIEVYTSPGGD
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2992. .4668
2992. .4668
2992. .4668
79ene="PE_PGRS"
2092. .4668
70ne="Rv1983, (MTCY39.36C), len: 558; Member of M.
7note="Rv1983, (MTCY39.36C), contains PS00141 Eukaryotic and viral aspartyl proteases active site; similar to MTCY130.10C, (43.3% identity in 522 aa overlap)"
small subunit, len: 322, highly similar to RIR4_SALTY P17424, ribonucleoside-diphosphate reductase (319 aa) FASTA scores, opt: 1402, ~scores: 1716.0, E(): 0, (66.0% identity in 315 aa overlap); Also similar to Rv3048c, (MTV012.63c); containsPS00368 Ribonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="PS00141 Eukaryotic and viral aspartyl proteases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="agga, potential rbs upstream of Rv1981c"
complement(2161, 2580)
/gene="Rv1982c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTCQVNPAVRAALDPGAGENHDFFSGSGSSYVMGTHQPTTDTDWDF'
complement(1589.~.1636)
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/protein_id="CAA98401.1"
/db_xref="G1:1403473"
/db_xref="SWISS-PROT:Q10874"
                                                                                                                                                                                                                                reductase small subunit signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SWISS-PROT:Q10840"
                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA98381.1"
/db_xref="GI:1403474"
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/transl_table=11
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/gene="PE_PGRS"
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Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CB10 ISA Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
On Jun 27, 1998 this sequence version replaced gi:1403436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSDPAYNIN'SLPSYYDDOKSLENY AQTROKFLSAATSSTPREAPYELNITSATYOS
AIPPRGTQAVVLKVYQNAGGTHPTTTYKAFDWDQAYRKPITYDTLWQADTDPLPVVFP
IVQGELSKQTGQQVSIAPNAGLDPVNYQNFAVTNDGVIFFFNPGELLPEAAGPTQVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              URLL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position g + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome blinding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"MRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQ
                                         Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squres, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Rv1980c, (MTCY39.39), len: 228, mpt64 identical to MPB6_MYCBO P19996 immunogenic protein mpb64/mpt64 (228 aa) Similar to Rv3036c, (MTV012.51c)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(968. .1936)
/gene="nrdf"
/nrcv39.38), ribonucleotide reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                              Deciphering the biology of Mycobacterium tuberculosis from the
         Basham, D., Brown, D., Chillingworth, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(787. .791)
/note="ggagg, potential rbs upstream of Rv1980c"
complement(968. .1936)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Erratum:[[published errâtum appears in Nature 1998 Nov
12,396(6707):190]]

    .38500 /
/organism="Mycobacterium tuberculosis"

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/strain-"H37Rv"
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/protein_id="CAA98382.1"
/db_xref="GI:1d03475"
/db_xref="SWISS-PROT:P19996"
                                                                                                                                                                                                                                                                                                                                                       complete genome sequence
Nature 393 (6685), 537-544 (1998)
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/clone="Y39"
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    Tekaia, F., Badcock, K.,
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(bases 1 to 38500)
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/bb_xref="G1:3401947"
/translation="WAAPVPAAPHFQPEAAAPAARLTAAYTLITVVGLACLSWLVIR
TDDBARMADRYDEMRRASVAASLYYYEDDRIRSAGPAEHRSLVLSLVIGAGALTALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB011413 12070 bp DNA BCT 07-AUG-1998 Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycescaess 1 to 12070)
                                                                                                                                                                                                                                                                                                                            5973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5853
                             6212 ACCGAGCGGAACCCGGTGCCGGGTGCACCCGCTGGGTGAAATGCGCTACCTA 6153
                                                                                                                                                                                                                                                                                                                                                                                                         6092 GCGGCTAAAGCTCCGTCACTGGCGTGGAATCGTGACGATGGGCTGCAGGACATGTTGGTG 6033
                                                                                           546
                                                                                                                                                                                                                                                                                                                                                                          664 tttggtgaggcaattcgccgaggccttggttggggacttcttcccgaaacccaagctgct 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      724 cccatgctaaaagcaggagaagtgatcctcctcgatgagatacccattgacacaccgatg 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (23-FEB-1998) to the DDBJ/EMBL/GenBank databases. To
Umeyama, University of Tokyo, Department of Agriculture and L.
Sciences, Yayoi 1-1. Bunkyo.ku, Tokyo 113, Japan
(E-mail:aa67103@hongo.ecc.u-tokyo.ac.jp, Tel:+81-3-3812-2111)
    cgtgaagctaatcccgtggcgggatgtgaagtagtagaacttggaaccatgcgccacttg
                                                                                                                                                                                                                                                                                   cg---cgtcgatggtcctgtggggggggggggggtatccattgtcccgtcggcggaaggt
                                                                                                                                       6152 CCAGTGGCCAGCAGGCCATTCGTCCAGCGCCATCTATCCGACGGGTTCACTGCCGCGGG
                                                                                              gccattgcaaccccctcattgcgggatgcctacatggttgatgggaaactagattgggct
                                                                                                                                                                                                                                                                                                         5912 TCTCCGCTTGCCGATGGATCGTTCGTACGGGTCTGCGACATACACCTCGACGTCCCTCTC
                                                                                                                                                                                     547 gcgatgcccgtcttacgcttcggtcccaaagatgtgcttcaagaccgtgacctggacggg
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Unpublished (1998)
Location/Qualifiers
1. 12070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:1911"
complement(2660. .3511)
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Streptomyces griseus DNA.
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AB011413.1
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VERSION
KEYWORDS
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TITLE
JOURNAL
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                                                                                           Qγ
                                         /note="Rv1984c, (MTCY39.35), len: 217. Probable cutinase precursor with N-terminal signal sequence, , similarity to CUTI_ALTBR P41744 cutinase precursor, (209 aa) FRSTA scores.opt: 283, z-score: 322.0, E(): 2.2e-11, (32.6% identity in193 aa overlap). Also similar to M. tuberculosis Rv3452, Rv3451, Rv2301, Rv1758, Rv3724."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jobbe "K1985C, (MTCX39.34), len: 303, LysR family member similar to many regulatory proteins, especially ICIA_ECOLI P24194, chromosome initiation inhibitor, (297 aa), and P94632 LYSINE EXPORT REGULATOR PROTEIN. (290 aa). FASTA scores, P94632 LYSINE EXPORT REGULATOR PROTEIN opt: 705 z-score: 850.6 E(): 0, 42.7% identity in 288 aa overlap; and ICIA_ECOLI P24194 opt: 520, z-score: 632.5, E(): 1.1e-28, (35.8% identity in 285 aa overlap); contains PS00044 Bacterial regulatory proteins, lysR family signature. Also contains helix-turn-helix motif at aa
                                                                                                                                                                                                                                                                                                    /db_xref="SWISS-PROT:Q10837"
/translation="MTPRSLVRIVGVVVATTLALVSAPAGGRAAHADPCSDIAVVFAR
                                                                                                                                                                                                                                                                                                                                               GTHQASGLGDVGEAFVDSLTSQVGGRGIGVYAVNYPASDDYRASASNGSDDASAHIQR
TVASCPNTRIVLGGYSQGATVIDLSTSAMPPAVADHVAAVALFGEPSSGFSSMLWGGG
SLPTIGPLYSSKTINLCAPDDPICTGGGNIMAHVSYVQSGMTSQAATFAANRLDHAG"
complemen (4950, 4987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGGTGCTGGTCAGGGAAAAGCCATGTCGGGCGACGACCGCAGGTATCCCGCTGTTG 6444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTCGCCCGTGTTCGACG------GTCTCGGCGACGTCCTGCTCGACGTTCGGATC 6273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctttccatttcccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgagtgttggtatcgcgccccaaccggccaaagcaaccgaagcgggtgaagtccttgtg 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gaagatgaagcgcacacattatccttgctgcggcgtggagatgttttaggagcggtaacc 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 121; DB 3; Length 38500;
Pred. No. 2.2e-23;
0; Mismatches 410; Indels 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PS00155 Cutinase, serine active site"
complement(5739 6650)
                                                                                                                                                                                  /codon_start=1
/transl_table=11
/product="hypothetical protein Rv1984c"
/protein_id="CAA98399.1"
/db_xref="GI:1403471"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-43, (+5.52 SD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Rv1984c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.9%;
Similarity 49.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Matches
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6340 CAGGTGCGGACCCTGCTGGCCGTGGTCGACGAAGGCACCTTCGACTCGGCGGCGACCGCC 6281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctttccatttcccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gatgaagcgcacacattatccttgctgcggcgtggagatgttttaggagcggtaacccgt 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5802 AGCTGATCGGCGAAGCTCCGGTGGTCTGCTTCGACAGGCGCGATCTCCAGGACGCCT
                                                                           caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc
                                                                                                                                                                                                                                                 133 cgagtgttggtatcgcgcacccaaccggccaaagcaaccgaagcgggtgaagtccttgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 cctcccgtgttcaacgaggtagcttcttgggggtggagcaacgctcacgctgcgcttggaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5982 GACCAGGACCATACGGCCGCCTGCTGCGGGAGGGGCTGGCGATGGCCGCGGTGACCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 gaagctaatcccgtggcgggatgtgaagtagtagaacttggaaccatgcgccacttggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       550 atg------cecqtettacgetteggteceaaagatgtgetteaagacegtg
                                                                                                                                                                                                                                                                                                                                     193 caage---agegeggaaaatggtgttgetgeaageagaaactaaagegeaactatetgga
                                                                                                                                                                                                                                                                                                                                                                                                                         cgccttgctgaaatcccgttaaccatcgccatcaacgcagattcgctatccacatggttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490 attgcaacccctcattgcgggatgcctacatggttgatgggaaactagattgggctgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    596 acctggacgggcgcgtcgatggtcctgtggggcgcaggcgcgtatccattgtcccgtcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5742 TCGTGCGCCGGGCCCCGGCCCGGCCGGCCGAGCGCCCGTCGCCACCTGGTACCCACCT
                                                                                                                                                                                                                                                                                                                                                                              6160 CTCGCCCGCCAGCTGGCCAGGCTGGAGCACGAGGCGCAGGCGCGCTCGGGATGTCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6100 CCGGCCGAGCCGACGCTCTGCCGATCGCGGTGAACTCCGATTCCCTGGCGACCTGG--T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5862 TGGCCAGTCCCGGTTTCGCCGGTGGCTGGGACGGCGGGGACGGCACCGCGTTGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5682 CGGAGGGGTTCGCGAACGCCGTGGCGTCGGGGATGGGCTGGGGCATGGTGCCCGAGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          716 aagctgctcccatgctaaaagcaggagaagtgatcctcctcg---atgagatacccattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5622 AGGCGGAGCCGTTGCTGAGCGACGGCCGGCTGGTGCGGCTCGCCCTGAGCCCACCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                             Indels
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                             424;
         Pred. No. 7.7e-20
                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       833 acgccgtcgttgatgcagcaatcgagggatt 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ribose phosphate isomerase A. Escherichia coli.
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                             ;
    48.8%;
                           425; Conservative
    Best Local Similarity
                             Matches
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ECRPIAA/c
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VERSION
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PRIRRAADRWADVVENLLTRGRLEAGRTSYGRSRLRLDQLVEEVCAELPEGGPGLESR
LEESVVEADAALVRVAVRNLLDNAVRHGPGSRGAAGRGRTAGDRVRTGVRVADRGPAV
                                                                                                                                                                                                                                          /translation-"MRVLVEDDDDLRDVIGAGLRDGGFAWDCASDWPEADVLLHLSA
ROCVVLDRWYPSGDTLAPLEGRRRAGWSVPUCLTALDSLDSPERLRGLESGADDVLAKP
FSWRELVLEVRGIGSRASARLPSFLGCADVWDDVARHEVRRGGVLLSLSFRFYAVLOO
LLVHRDTVVTRTGLLEHCWDEMADPVSNVVDAVVGLRRKLGSPGLVHTVRGGGFLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MATQALGTALRLGVFDRIGTGELRAEALAGSLGTHPRATLRLLR
ALAGLQLLSPEPEPARTTAAGNVLARDAPGTWAMRAWFTDPVMLRGWDLJDESVRT
GETTFDTVGTDFFGHLRAHPELSAARONGGTRLTAFTVPHYVDFGRFQRLVDIG
GGDGTLLASILRAHQPERGVLFDTAEGLAGAPRRLAREGLDGRYTLETGDFFRSAPAG
GDLYLLNSIIHDWDDAVRGHLRHIRDVIPDHGSLLIVEPVLPATVPADRPDNVYLSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MTTVAAYAAPRAKAPLERTTIERRPVGEFDILIDIKFAGICHSD
IHQARDGWGEGIFPWYPGHEIAGIVAETGPGVTRFKVGDRVGVGCWVDSCGTCDACLM
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FREIALDEAAPLLAG
ITYSPLERRAGGFGKKVAVULGGYSTHLVYTEKFALS:
PEGIALDEAAPLLAG
ADHYYATGDPRYFEAGTOKVVLGSTVSAVALDFGATALRTEGTLVNVGAPEEPVSL
NLFSLILGNRSIAGSAIGGIEETQGMLDFCAVHGLGAEIEVIGAGQVNEAYERVLASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAA32134.1"
/db_xref="GI:3401951"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HDHPFFAPVGDDLHDPLLVAEAMRQAAMLAFHAGYGIPLGYHFLLTELDYVCHPEHLG
VGGEPFEIGLEVFCSDLKWRAGLPAGORVGMAYHGDRLAATGVAAATFSTPRAYRRM
RGDVPVEGISLPETAPPASPARAN
RGDVPVEGISLPETAPPASPARANFEDVVL.GGTGREGVWELRVDFHPTLFQRPND
HVPGMLLLEAARQAACLVAGPAGIVPVEARTFRFRYSEFGSPCWIGAVVQPGADEDTY
                                                                                                             function="two-component regulator protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            function-"alcohol dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NMLVNVGGRERTADDFAALCTAGGFACGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="regulator protein"
                                                                                                                                                                                                                                                                                                                                                     complement(4333. .>5250)
/function="methyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LESPALAAVAEAVAAEAAEALDEAPPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVRVTGHQDGETVFSTVLSGPRAHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAA32132.1"
/db_xref="GI:3401949"
                                                                                                                                                                                                   /protein_id="BAA32131.1"
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/db_xref="GI:3401952"
                                                                                          complement(3523. .>4197)
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                                                                                                                                                        /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
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/transl_table=11
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                                                                                                                                                                                 /product="Orf3"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"Orf4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Orf8"
                                                                                                                                   /codon_start=1
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5863

489

549

5803

595

5743

655

5623

772

715

5563

ORGANISM

Length 12070;

DB 1;

Score 108.6;

12.48;

Query Match

11

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/translation="MKRPDYRTLQALDAVIRERGFERAAQKLCITQSAVSQRIKQLEN
MFGQPLLVRTVPPRFPTEQGGKLLALLRQVELLEEBWLGDEGGSTPLLLSLAVNADSL
ATWLLPALAPVLADSPIRINLQVEDETRYQERLRRGEVVGAVSIQHQALPSCLVDKLG
ALDYLFVSSR PFABEK FPNGVTRSALLKAPVVAFDHLDDMHQAFLQQNFDLPFGSVPC
HIVNSSEAFVQLARQGTTCCMIPHLQIEKELASGELIDLTPGLFQRRMLYWHRFAPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECOICIA 1815 bp DNA BCT 06-MAR-1995
E.coli chromosome initiation inhibitor (iciA) gene, complete cds.
M62865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.

1 (bases 1 to 1815)
Thony, B., Hwang, D.S., Fradkin, L. and Kornberg, A.
icia, an Escherichia coli gene encoding a specific inhibitor of chromosomal initiation of replication in vitro
Proc. Natl. Acad. Sci. U.S.A. 88 (10), 4066-4070 (1991)
91239508
                                                                                                                                 275 tegecateaaegeagattegetateeaetggttteeteeegtgtteaaegaggtagett 334
                                                                                                                                                          335 cttggggtggagcaacgctcacgctgcgcttggaagatgaagcgcacacattatccttgc 394
                                                                                                                                                                                                                                                                                          395 tgcggcgtggagatgttttaggagcggtaacccgtgaagctaatcccgtggcgggatgtg 454
                                                                                                                                                                                                                                                                                                                                126 TGCGCCGCGGCGAAGTGGTCGGCGGGGGGGTGATTCAACATCAGGCGCTGCCGAGTTGTC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="Inhibitor of oric replication in vitro"
/product="chromosome initiation inhibitor"
/protein_id="AAA62780.1"
/db_xref="G1:146436"
                                                                                             TGCTGGAAGAAGAGTGGCTGGGCGATGAACAAACCGGTTCGACTCCGCTGCTGCTTTCAC
                                                          tgctgcaagcagaaactaaagcgcaactatctggacgccttgctgaaatcccgttaacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome initiation inhibitor; iciA gene.
E.coli (strain W3110) DNA, (Kohara library) clone IA2
('miniset'-set No. 471).
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62.8 min. on K-12 map; kb coordinate 3974.
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No. 1.9e-12;
                                                                                                                                                                                                                                                                                                                                                                       aagtagtagaacttggaaccatgcgccattggccat 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_lib="E.coli Kohara"
/map="62.8 min. on K-12 ma"
650. .1543

    1815
    organism="Escherichia"

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/strain="K-12"
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650. .1543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        650. .1543
/gene="iciA"
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Best Local Similarity
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ORIGIN
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                                                                                             306
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KEYWORDS
SOURCE
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ATWLLAPALAPVLADSPIRLNLQVEDETRTQERLRRGEVVGAVSTQHQALPSCLVDKLG
ALDYLFVSSKPFAEKY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation-"MTQDELKKAVGWAALQYVQPGTIVGVGTGSTAAHFIDALGTWKG
GIEGAVSSDASTEKLKSLG1HYPDIAEVDSLGIYVDGADEINGHWQMTKGGGAALTR
EKIIASVAREFIOTADASKOVDILGKFPLPFUIPWARSAVARQLVKLGGRPEYRGGV
VTDNGNVILDVHGMEILDPIAMENAINAIPGVVTVGLFGANRGADVALIGTPDGYKTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'translation="MKRPDYRTLQALDAVIRERGFERAAQKLCITQSAVSQRIKQLEN
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Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                  1 (bases 1 to 1804)
Hove-bensen, B. and Maigaard, M.
Escherichia coli rpia gene encoding ribose phosphate isomerase
J. Bacteriol. 175 (17), 5628-5635 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           486 TGATACGTGAACGAGGATTTGAGCGCGGGGCACAAAAGCTGTGCATTACACAATCAGCCG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgagtcagcgcgttaaagctctcgagcatcacgtgggtcgagtgttggtatcgcgcaccc 154
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                                                                                                                                                                      Direct Submission
Submitted (23-APR-1993) B. Hove-Jensen, Dept. of Biological
Chemistry, Univ. Inst. of Mol. Biology, Solvgade 83, Dk-1307
Copenhagen, DENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tcattgatgaaggcagcttcgaaggcgcctccttagccctttccatttcccctcggcgg
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Pred. No. 1.9e-12;
); Mismatches 234; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="ribose 5-phosphate isomerase"
/protein_id="CAA51509.1"
/db_xref="G1:405640"
                                                                                                                                                                                                                                                                                          /organism="Escherichia coli"
/strain="K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'db_xref="SWISS-PROT:P24194"
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'db_xref="G1:405639"
                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                                                                                                           complement(<1. .529)
/gene="iciA"
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/codon_start=1
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 /map="63 min"
complement(1. .529)
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/transl_table=11
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/gene="rpiA"
44. .946
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/gene="rpiA"
a 448 c
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/gene="rpiA"
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'gene="rpiA"
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                                                                                                                               2 (bases 1 to 1804)
Hove-Jensen, B.
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23; Conservative
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Matches 223;
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ORIGIN
                                                                                       JOURNAL
MEDLINE
REFERENCE
                                                                                                                                                                      TITLE
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                                    REFERENCE
                                                                                                                                                      AUTHORS
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/translation="MAKVSLEKDKIKFLLVEGVHQKALESLRAAGYTNIEFHKGALDD
EQLKESIRDAHFIGLRSRTHLTEDVINAAEKLVAIGCFCIGTNQVDLDAAAKRGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATWILPALAPVLADSPIRLNLQVEDETRTQERLRRGEVVGÄVSIQHQALPSCLVDKLG
ALDYLLVSSREPAEKTPROTYRSALLKAPVVAFDHLDDMHQAFLQQNFDLPPGSVPC
HIVBSSEAFVQLAGGTTCCMIPHLQIEKELASGELIDLTPGLFQRRMLYWHRFAPES
RMMRKVTDALLDYGHKVLRQD"
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QHRBNLLAARVNAARVRATLGEISDALEVAEDRYLVPSQCYTGVIAOSYHQSRKSASE
FDAIVAQTEQFLADNGRRPRILIAKMGQDGHDRGAKVIASAYSDLGFDVDLSPMFSTP
EEIARLAVENDVHVGASSLAAGHKTLIPELVEALKKWGREDICVVAGGVIPPQDYAF
LQERGVAAIYGPGTPMLDSVRDVLNLISQHHD"
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LGGASQRARELMLLCEAAGYDVYVETVGYGQSETEYARMVDCFISLQIAGGDDLQG
IKKGLMEVADALLVINKDDGDNHTWVAIARHMYESALHILRRKYDEWQPRVLTCSALEK
RGIDEIWHAIIDFWALTSGRLGOVRQQQSVEWLRKGTRRSTESEVRE"
1615 c 1550 g 1413 t
                                                                                                                                                                                                                                                 /translation="MRVKFHTGETIMTQDELKKAVGWAALQYVQPGTIVGVGTGSTA
HFIDALGYMKGQIEGAVSSDASTBKLKSLGHHYBDLMBVDSIGIYVOGADEINKHH
QMIKGGGAALTREKITASVARKFICTADASKQYDLLGKFPLPYEVIPMARSAVRQLY
KLGGRPEYRQGVYTDNGNVILDVHGMEILDPIAMENAINAIRGADVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="msnvqewqqiankelsrrektvdslvhqtabgiairplytyedd
DNLEVTGTLPGLPPYYRGPRATMYTAQPWTIRQYAGSTAKESNAFYRRNLAAGQKGL
SVAFDLATHRGYDSDNPRVAGDVGKAGYAIDYVEDMKVLFDQIPLDKMSVSWTWMGAV
LPVLAFYIVAAEEGGWPPKLTGTIONDILKEYLCRNTYIYTPPRPSMRIIADIIAWGS
GNMPRRNIISISGYAWPDRAGANCVQOVARTLADGIEYIKAAISAGLKIDDFAPRLSFF
FGIGMDLFMNVAMLRAARYLWSEAVSGFGAQDPKSLALRTHCQTSGWSLTEQDPYNNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mKRPDYRTLQALDAVIRERGFERAAQKLCITQSAVSQRIKQLEN
MFGQPLLVRTVPPRPTEQGQKLLALLRQVELLEEEWLGDEQTGSTPLLLSLAVNADSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRTTIEALAATLGGTQSLHTNVFDEALGLPTDFSARIARNTQIIIQEESELCRTVDPL
AGSYYIESLTDQIVKQARAIIQQIDEAGGMAKAIEAGLPKRMIEEASAREQSLIDQGK
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Pred. No. 1.8e-12;
); Mismatches 234;
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/db_xref="G1:42945"
/db_xref="SWISS-PROT:P27253"
          db_xref="SWISS-PROT:P08328"
                                                                                                                                                                                                                          /db_xref="SWISS-PROT:P27252"
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/db_xref="G1:42946"
/db_xref="SWISS-PROT:P27254"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="inhibitor of c
/protein_id="CAA47310.1"
/db_xref="GI:42944"
                                                                                                                                                                              /protein_id="CAA47309.1"
/db_xref="GI:42943"
                                                                          complement(554. .1249)
/note="orf1"
                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="iciA orf"
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/transl_table=11
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/note="sbm orf"
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                                                                                                                                                                                                                                                                                                                                                        LIGTPDGVKTIVK"
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/gene="iciA"
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/gene="iciA"
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/note="orf2"
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Best Local 9
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ORIGIN
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Escherichia.
1 (bases 1 to 6055)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               993 CTGATTCGCCTATCCGCCTCAACTTGCAGGTAGAAGATGAAACCCGCACTCAGGAACGTC 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1053 receccecedadrecrescesceses arteracarcas escentes contrated 1112
                                                                                                    693 TGATACGTGAACGAGGATTTGAGCGCGCGCACAAAAGCTGTGCATTACACAATCAGCCG 752
                                                                                                                                                     tgagtcagcgcgttaaagctctcgagcatcacgtgggtcgagtgttggtatcgcgcaccc 154
                                                                                                                                                                                                753 TCTCACAGCGCATTAAGCAACTGGAAAATATGTTCGGGCAGCCGCTGTTGGTGCGTACCG 812
                                                                                                                                                                                                                                                    aaccggccaaagcaaccgaagcgggtgaagtccttgtgcaagcagcgggaaaatggtgt 214
                                                                                                                                                                                                                                                                                          813 TACCGCCGCCCCGACGGAACAAGGCCAAAAACTGCTGGCACTGCTGCCGCCAGGTGT 872
                                                                                                                                                                                                                                                                                                                                                   tgctgcaagcagaaactaaagcgcaactatctggacgccttgctgaaatcccgttaacca 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                               tegecateaacgeagattegetatecacatggttteeteeegtgtteaacgaggtagett 334
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2 (bases 1 to 6055)
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                                                   35 tcattgatgaaggcagcttcgaaggcgcctccttagccctttccatttccccctcggcgg
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/protein_id="CAA47308.1"
/db_xref="GI:42942"
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/clone_lib="lambda EMBL three"
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/note="partial of serA orf"
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/organism="Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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Escherichia.
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Plunkett, G. III.
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University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHRR). The entire sequence was independently.

Getermined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, Kindly supplied by Marx Barcadowsky. Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos. unique ID nos. for the genes in the E. coli Genetic Stock Center (GGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome to Site noncations are periodically updated; this is version M54. No sequence changes. Annotation abates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assignments coach gene (protein or RNA-encoding) are now designated as gene synonyms instead of hames.
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MFGQPLLVBRVPPRRPTEOGGKLLALLRQVELLEEBWLGDEOTGSTPLLLSLAVNADSL
ALDYLLPALAPVLADSPIRLNLQVEDETRYQERLRRGEVVGAVSIQHQALPSGLVDKLG
ALDYLEVSSRFPREYFRVYTRSALLKAPVVAFDHLDDMHQAFLQONFDLPRESVPR
HIVNSSEAFVQLARQGTTCCMIPHLQIEKELASGELIDLTPGLFQRRMLYWHRFAPES
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restriction/modification"
/note="0.29; 100 pct identical to ICIA_ECOLI SW: P24194;
CG Site No. 28646"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="enzyme; Degradation of small molecules: Fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="o714; 99 pct identical to SBM_ECOLI SW: P27253"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1045. .1072
/note="factor Sigma70; predicted +1 start at 3058751"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted +1 start at 3057674"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="factor Sigma70; predicted +1 start at 3057742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
/product="replication initiation inhibitor, binds 13-mers at OriC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product."methylmalonyl-CoA mutase (MCM)"
/protein_id="AAC75954.1"
/db_xref="GI:1789284"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Escherichia coli K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAC75953.1"
/db_xref="G1:1789283"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(9. .40)
/note="factor Sigma70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:83333"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sub_strain="MG1655"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101. .994
/gene="iciA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101. .994
/gene="iciA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1198. .3342
/gene="sbm"
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/gene="sbm"
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Gaps 94

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/function="putative regulator; Not classified"
/note="f303; This 303 aa ORF is 25 pct identical (11 gaps)
to 241 residues of an approx. 304 aa protein CYNR_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE005521 10367 bp DNA BCT 21-MAR-2001
Escherichia coli 0157:H7 EDL933 genome, contig 3 of 3, section 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dena, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apdaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R. Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                            /product="putative transcriptional regulator LYSR-type"
/protein_id="AAC75958.1"
/db_xref="GI:1789288"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 TGATACGTGAACGAGGATTTGAGCGCGCGCACAAAAGCTGTGCATTACACAATCAGCCG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgagtcagcgcgttaaagctctcgagcatcacgtgggtcgagtgttggtatcgcgcaccc 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgctgcaagcagaaactaaagcgcaactatctggacgccttgctgaaatcccgttaacca 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tegecateaaegeagattegetateeaeatggttteeteeegtgtteaaegaggtagett 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                504 TGCGCCGCGCGAAGTGCTCGGCGCGGTGAGTATTCAACATCAGGCGCTGCCGAGTTGTC 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 aaccggccaaagcaaccgaagcgggtgaagtccttgtgcaagcagcgggaaaatggtgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tgcggcgtggagatgttttaggagcggtaacccgtgaagctaatcccgtggcgggatgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tcattgatgaaggcagcttcgaaggcgcctccttagccctttccatttcccctcggcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cttgggggtggagcaacgctcacgcttggcaagatgaagcgcacacattatccttgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 CTGATTCGCCTATCCGCCTCAACTTGCAGGFAGAAGATGAAACCCGCACTCAGGAACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 TACCGCCGCCCCGACGGAACAAGGCCAAAAACTGCTGGCACTGCTGCGCCCAGGTGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 10362;
        HPMYRDYLHRYLENAPGGHIHHDLSHVFDLHRNLIATGSMLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 82.6; DB 1; Length 1
Pred. No. 1.7e-12;
0; Mismatches 234; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       564 TIGICGATAAACIIGGIGGCCICGACIAICIGIICGI 600
                                     complement(6625. .7536)
                                                                                                                     .7536)
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Escherichia coli 0157:H7 EDL933
                                                                                                                                               /gene="ygfI"
/function="putative
                                                                                                                     complement (6625.
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/transl_table=11
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                                                                                        /note="b2921"
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ilarity 48.8%;
Conservative
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Best Local S:
Matches 223
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AE005521
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                                     gene
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                                                                                                                     CDS
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RVICKVNKXLDHEDETDVLEIDNYWYRNEQISALERIRATRDDAAYAALANLTHAA
QHENLLAAAVNAARVRATLGEISDALEVAEDRYLVPSQCVTGVIAQSYHQSEKSASE
PDAIVAQTEQFLADHORRPRILIAKWGDGHRGAKVIASAYSDLGEPVDLSPRESTP
EEIARLAVENDYHVYGASSLAAGHKTLIPELVEALKKWGREDICVVAGGVIPPQDXAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation-"MINEATLAESIRRLRQGERATLAQAMTLVESRHPRHQALSTQLL
DAIMPYCGNTLRLGYTGTPGAGKSTFLEAFGMLLIREGLKVAVIAVDPSSPVTGGSIL
GDKTRNNDLARAEAAFIRPVESSGHLGGASQRARELMLLCEAAGYDVVIVETYGYGGSI
ETYDARWYDCFISLQIAGGDDLQGIKKGLMEVADLIVINKDDGDNHTNVAIRHNYE
SALHILRRKYDEWQPRYLTCSALEKRIDETWHAIIDFKTALTASGRLQQVRQQSVE
MLRKQTEEEVLNHLFANEDFDRYYRQTLLAVKNNTLSPRTGLRQLSEFIQTQYFD"
DNLEVTGTLPGLPPYVRGPRATMYTAQPWTIRQYAGFSTAKESNAFYRRNLAAGQKGL
SVAFDLATHRGYDSDNPRVAGDVGKAGVAIDTVEDMKVLFDQIPLDKMSVSMTMNGAV
LPVLAFYIVAAEEGGVTPDKLTGTIQNDILKEYLCRNTYIYPPKPSMRIIADIIAWCS
                                                                                   GNMPRENTISISGYHMGEAGANCVQQVAFTLADGIEYIKAAISAGLKIDDFAPRLSFF
FGIGMDLFMNVAMLRAARYLWSEAVSGFGAQDPKSLALRTHCQTSGWSLTEQDPYNNV
IRTTIEALAATLGGTQSLHTNAFDEALGLPTDFSARIARNTQIIIQEESELCRTVDPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MNLSRRNILIKGIFMSYQYVNVVTINKVAVIEFNYGRKLNALSK
VFIDDLMQALSDLNRPEIRCIILRAPSGSKVFSAGHDIHELPSGGRDPLSYDDPLRQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRMIOKFPKPIISMVEGSVWGGAFEMIMSSDLIIAASTSTFSWTPVNLGVPYNLVGÎH
NLTRDAGFHIVKELIFTASPITAQRALAVGILNHVVEVEELEDFTLOMAHHISEKAPL
AIAVIKEELRVLGEAHTMNSDEFERIQGMRRAVYDSEDYQEGMNAFLEKRKPNFVGH"
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VPPPMYFSEVLQESVVHLLETGKISGASASSLITASADSLKRITDNMPYFASRIYLRP
QEISNNPEIIRRLGVALLNCELEPTYGHANSTHVAGVDLMAGIGGSGDFERNAYLSI
FMAPSIAKEGKISTVVPMCSHVDHSEHSVKVIITEQGIADLRGLSPLQRARTIEDUCA
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VDLHLSEVAQMVNYGFFGDIDVAVIEASALAPDGRVWLTSGIGNAPTWLLRAKKVIIE
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/note="0492; This 492 aa ORF is 46 pct identical (7 gaps)
to 490 residues of an approx. 544 aa protein CATI_CLOKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="putative enzyme; Not classified"
/note="0275; This 275 aa ORF is 30 pct identical (6 gaps)
to 250 residues of an approx. 296 aa protein ECHM_RAT SW:
p14604"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="phenotype; Not classified"
/note="0331; 100 pct identical to YGFD_ECOLI SW:
P27254(257 aa) but has 25 additional N-ter aa 50
additional C-ter aa; orf2 of X66836"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative nucleotide-binding protein"
/protein_id="AAC75955.1"
/db_xref="GI:1789285"
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/protein_id="AAC75957.1"
/db_xref="GI:1789287"
                                                                                                                                                                                                                                                                                                               LQERGVAAIYGPGTPMLDSVRDVLNLISQHHD"
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/product="putative enzyme
/protein_id="AAC75956.1"
/db_xref="GI:1789286"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFNRHGARYPSYNTIVGSGENGCILHYTENECEMRDGDLVLIDAGCEYKGYAGDITRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="msaqpydiqifgrslryncppdqrdalnqaaddlnqrlqdlkrr
trytnteqlyfiaalnisyelaqekaktrdyaasmeqrirmloqtieqalleggrite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="putative enzyme; Not classified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="24247"
4855. 5184
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Strain MG1655: B2909"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="RNA; Macromolecule synthesis, modification:
Ribosomal and stable RNAs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="orf, hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Z4249"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4855. .5184
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/gene="ssrS"
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MG1655: B2906"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mQSVDVAIVGGGMVGLAVACGLQGSGLRVAVLEQRVPEPLAADA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPHLCSIVWSLSPEEAQRMQQASEDEFNRALNIAFDNRLGLCKVESARQVFPLTGRYA
RQFAAHRLALVGDAAHTIHPLAGQGVNLGFMDAAELIAELKRLHRQGKDIGQYIYLRR
YERSRKHSAALMLAGWQGFRDLFSGTNPVKKLLRDIGLKLADTLPGVKPQLIRQAMGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Menaquinone, ubiquinone" force "Residues 1 to 392 of 392 are 98.97 pct identical to residues 1 to 392 of 392 from Escherichia coli K-12 Strain MG1655: B2907"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="G1:12517437"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGADGANSWLRNKADIPLTFWDYQHHALVATIRTEEPHDAVARQVFHGEGILAFLPLS
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ADGTHSALATVCGVDWQQEPYEQLAVIANVATSVAHEGRAFERFTQHGPLAMLPMSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITHRTVLVGNAAQTLHPIAGQGFNLGMRDVMSLAETLTQAQERGEDMGDYGVLCRYQQ
RRQSDREATIGVTDSLVHLFANRWTPLVVGRNIGLMTMELFTPARDVLAQRTXGWVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RCSLVWCHPLERREEVLSWSDEKFCRELQSAFGWRLGKITHAGKRSAYPLALTHAARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macromolecule degradation: Degradation
                                                                                                                         2 (bases 1 to 10367)
Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Posta, G., Markett, J., Klink, S., Gregor, J., Kirkpatrick, H.A., Postai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Mach, R.A. and Blattner, F.R.
Direct Submission
Submitted (22-OCT-2000) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="enzyme; Biosynthesis of cofactors, carriers:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .10367
/organism="Escherichia coli 0157:H7 EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="orf, hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="enterohemorrhagic"
complement(357. .1559)
Nature 409 (6819), 529-533 (2001)
21074935
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/db_xref="taxon:155864"
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/function="enzyme;
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/transl_table=11
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/note="Z4244"
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RESULT 14
GELDTQPLIEQXWRAGKRVYLPVLHPFSÄGNLLFLNYHPQSELVMNRLKIHEPKLDVR
DVLPLSRLDVLITPLVAFDEYGQRLGMGGGFYDRTLQNWQHYKTQPVGYAHDCQLVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MAKVSLEKDKIKFLLVEGVHQKALESLRAAGYTNIEFHKGALDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQLKESIRDAHFIGLRSRTHLTEDVINAAEKLVAIGCFCIGTNOVDLDAAAKRGIPVF
NAPFSNTRSVAELVIGELLLLRGVPEANAKAHRGVWNKLAAGSFFBARGKKLGIIGYG
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                                                                   6267. .6659
/note-"0-island #118; Region of the EDL933 chromosome not
homologous to E. coli K-12 MG1655"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="enzyme; Amino acid biosynthesis: Serine"
/note="Residues 1 to 410 of 410 are 100.00 pct identical
to residues 1 to 410 of 410 from Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9386 TGATACGTGAACGAGGATTTGAGCGCGCGCGCACAAAAGCTGTGCATTACACAATCAGCCG 9445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCGTCGCGGCGAAGTGGTCGGCGCGGTGAGTATTCAACATCAGGCGCTGCCGAGTTGTC 9805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9566 TGCTGGAAGAAGAGTGGCTGGGCGATGAACAAACGGTTCGACTCCGCTGCTGCTTTCAC 9625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9446 TCTCACAGGGCATTAAGCAACTGGAAATATGTTCGGGCAGCCGCTGTTGGTGGTGCGTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 aaccggccaaagcaaccgaagcgggtgaagtccttgtgcaagcagcgggaaaatggtgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tegecateaaegeagattegetateeaeatggtteeteeegtgtteaaegaggtagett
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/protein_id="AAG58040.1"
/db_xref="GI:12517443"
                                                                                                                                                                                                                                                                                                                                              /protein_id-"AAG58039.1"
/box xref="GG1:1231742"
/translation-"MKWLSKSSVGDAPRIALIDIVDSLT"
complement(6814. .8046)
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                                                                                                                                                                                                                                                   /function="orf; Unknown function"
/note="No significant matches"
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                                                   LPVEEWDIPLPAVVTPSKVWEW"
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/transl_table=11
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                                                                                                                                                   6396. .6476
/gene="24250"
6396. .6476
/gene="24250"
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Consensus quality: 319973 bases at least Q40.
Consensus quality: 373739 bases at least Q30
Consensus quality: 373739 bases at least Q30
Consensus quality: 373739 bases at least Q30
Consensus quality: 377200 bases at least Q20
Estimated insert size: 180000; pulse field gel estimation
Quality coverage: 10.25 in Q20 bases; pulse field gel estimation
Quality coverage: 4.32 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 179 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jun 29, 2000 this sequence version replaced gi:6980223.
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                  AC020850 444882 bp DNA HTG 12-JUL-2000
Mus musculus clone RP21-460J8, WORKING DRAFT SEQUENCE, 179
                              LOCUS AC020850 Accession AC020850
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Center clone name: RPCI-21_460J8
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1258
2406
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                                             Fragment Name
AC020850_0
AC020850_1
AC020850_3
AC020850_3
AC020850_4
AC020850_1
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AC020850_0/c
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in length

11762 gap of unknown length 13127 contig of 1365 be in length 1327 gap of unknown length 1327 gap of unknown length 1327 gap of unknown length 13433 gap of unknown length 15188 gap of unknown length 15188 gap of unknown length 15189 gap of unknown length 15182 gap of unknown length 15182 gap of unknown length 15182 gap of unknown length 15183 gap of unknown length 15185 gap of unknown length 15186 gap of unknown length 15185 gap of unknown length	60981: contig of 1175 61081: gap of unknown 62213: contig of 1132 62313: gap of unknown 63704: contig of 1391 65623: contig of 1719 66821: contig of 1198 66921: gap of unknown 67957: contig of 1198 68057: gap of unknown 63037: contig of 1036	69461: contig 70606: contig 70506: gap of 72136: contig 7236: gap of 73864: contig 7364: gap of 75021: contig 75121: gap of 7527: gap of 7627: contig 78249: gap of 7827: contig 7827: contig 7827: contig 7827: gap of 80797: contig 80897: gap of 80897: gap of	contig of 1011 gap of unknown contig of 1364 gap of unknown contig of 1529 gap of unknown contig of 1186 gap of unknown contig of 1121 gap of unknown contig of 1121 gap of unknown contig of 1131 gap of unknown contig of 1331	Query Match 9.5%; Score 82.6; DB 66; Length 110000; Best Local Similarity 48.8%; Pred. No. 1.5e-12; Matches 223; Conservative 0; Mismatches 234; Indels 0; Gaps 0; Qy 35 tcattgatgaaggcagcttcgaaggcgctccttagcctttccatttcccctcggggg 94 Indels 0; Indels 0; Gaps 0; Qy 11
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/protein_id="AAA69074.1"
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                                                                                                                                      complement(559.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"MAIALVTGGSRGIGRATALLLAQEGYTVAVNYQQNLHAAQEVMN
LITQAGGRAFVLQADISDENQVVAMFTAIDQHDEPLAALVNNAGILFTQCTVE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (01-JUN-1995) Guy Plunkett, Laboratory of Genetics,
Submitted (01-JUN-1995) Guy Plunkett, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
This sequence was determined as part of the E. coll Genome Project
(Frederick R. Blattner, director) at the University of
Wisconsin-Madison. Supported by award HG00301 from the NIH Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Project. The entire sequence was independently determined from E. coll MG1655; overlaps with other sequence determinations are annotated. This entry should be considered somewhat provisional; it will be updated and merged with others at a later
                                                                                                                                      96549 TGCGCCGCGCGCAAAGTGGTCGCCCGCGCGCGCGCTGCCCGCTGCCCGATTTCAACATCAGGCCCTGCCCGAATTTCAACATCAGCCTGCCCGAATTTCAACATCAGCCTGCCCGAATTTC 96490
                                                                  96729 TGCTGGAAGAAGAGTGGCTGGGCCGATGAACAAACCGGTTCGACTCCGCTGCTGCTTTCAC 96670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                        tgctgcaagcagaaactaaaagcgcaactatctggacgccttgctgaaatcccgttaacca 274
                                                                                                                tegecateaaegeagattegetateeaeatggttteeteeegtgtteaaegaggtagett 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1995
68 minutes.
                                                                                                                                                                                                         cttggggtggagcaacgctcacgctgcgcttggaagatgaagcgcacacttatccttgc
                                                                                                                                                                                                                                                       96609 CTGATTCGCCTATCCGCCTCAACTTGCAGGTAGAAGATGAAACCCGCACTCAGGAACGTC
                                                                                                                                                                                                                                                                                                   tgcggcgtggagatgttttaggagcggtaacccgtgaagctaatcccgtggcgggatgtg
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/note="similar to GenBank Accession Number D21144
(ECOPYUI8)"
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Escherichia coli K-12 genome; approximately 65 to
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/map="approximately 65 to 68 minutes"
                                                                                                                                                                                                                                                                                                                                                                                                                                               96489 TTGTCGATAAACTTGGTGCGCTCGACTATCTGTTCGT 96453
                                                                                                                                                                                                                                                                                                                                                                                                   455 aagtagtagaacttggaaccatgcgccacttggccat 491

    .141744
    /organism="Escherichia coli"

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/db_xref="GI:882432"
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1 (bases 1 to 87107)
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QIEGM_TRQGAVSAAPFGSASILPISWMYIRWMGAEGLKKASQVAILNANYIASRLQD
AFPYLYTGROGRVAHECILDIRPLKEETGISELDIARRLIDYGFHAFTWSFPYAGTLM
YEPTESESKVELDRFIDAMAIRAETRAETDQVKAGVWPLEDNPLVNAPHIQSELVAEWAHP
YSREVAVFPAGVADRYKWPTVKRLDDVYGDRNLFCSCVPISEYQ"
COMPLEMENT(3551. .3940)
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CYSQVLLANTASLYAYYHGYOLKRINKIHKLIDILAAGLOQKGKLKRHSHAYPDTLC
VEVADKAGYLTRAABAINLRSDILANVÇITLDETTRENVMOLFNVLLGDNHGLDID
TLDKDVAHDSRSIQPAMLRDDEILTHPVFNRYHSETEMMRYMHSLERKDLALNQAMIP
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NDAQRQAVEGMKPFFGVQAGDLFIATTGYTGEAGYEIALPNEKAADFWRALVEAGVKP
CGLGARDTLRLEAGMNLYGQEMDETISPLAANMGWTIAWEPADRDFIGREALEVQREH
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LENDGWYTAYTPYQPEVSQGRLEALLNFQQVTLDLTGLDMASASLLDEATAAAEAMAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKRVXKLKNANRFFVASDVHPQTLDVVRTRAETFGFEV IVDDAQKVLDHQDVFGVLLQ
QVGTTGEIHDYTALISELKSRKIVVSVAADIMALVLLTAPGKQGADIVFGSAQRFGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGSCTMKLNAAAEMIPITWPEFAELHPFCPPEQAEGYQQMIAQUADWLVKLTGYDAVC
MQPNSGAQGEYAGLLAIRHYHESRNEGHRDICLIPASAHGTNPASAHMAGMQVVVVAC
DKNGNIDLTDLRAKAEQAGDNLSCIMVTYPSTHGVYEETIREVCEVVHQFGGQVYLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANMNAQVGITSPGFIGADVSHLNLHKTFCIPHGGGGPGMGPIGVKAHLAPFVPGHSVV
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LPEVGATVSAGDDCAVAESVKAASDIYAPVSGEIVAVNDALSDSPELVNSEPYAGGWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MAQQTPLYEQHTLCGARMVDFHGWMMPLHYGSQIDEHHAVRTDA
GMFDVSHMTIVDLRGSRTREFLRYLLANDVAKLTKSGKALYSGMLNASGGVIDDLIVY
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GETALVQIRNREMPVKVTKPVFVRNGKAVA"
complement(318. .3634)
/note="similar to GenBank Accession Number L20872
(ECOGCWHP); bases 3318 to 3438 differ from the sequence presented here, as well as from X73958 and D21144"
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                                                                                                                                                                complement(559. .3432)
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/codon_start=1
/transl_table=11
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                                                                               IGADGANSWLRNKADIPLTFWDYQHHALVATIRTEEPHDAVARQVFHGEGILAFLPLS
DPHLCSIVWSLSPEEAQRWQQASEDEFNRALNIAFDNRLGLCKVESARQVFPLTGRYA
                                                                                                                                RQFASHRLALVGDAAHTIHPLAGQGVNLGFMDAAELIAELKRLHRQGKDIGQYIYLRR
YERSRKHSAALMLAGMQGFRDLFSGTNPAKKLLRDIGLKLADTLPGVKPQLIRQAMGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDGRAIALAAGTCQQLARIGVWQSLADCATAITTVHVSDRGHAGFVTLAAEDYQLAAL
GQVVELHNVGQRLFALLRKAAGGVTLHCPDRVANVARTQSHVEVTLESGETLTGRVLVA
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SCSLWWCHPLERREEVLSWSDEKFCRELQSAFGWRLGKITHGKRSAYPLALTHARS
ITHRTVLVGNAAQTLHPLAGOGFNLGMRDVWSLTLTLTQAQERGEDMGDYGVLCRYQO
RRQSDREATIGVPDSLYHLEANRWAPLVVGRAIGLMTWBLFFPARDVLAQRTGWVDG
RRQSDREATIGVPDSLYHLEANRWAPLVVGRAIGLMTWBLFFPARDVLAQRTGWVDA
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FPVNGKFTQAQREIYDIVLESLETSLRLYRPGTSILEVTGEVVRIMVSGLVKLGILKG
DVDELIAQNAHRPFFMHGLSHWLGLDVHDVGVYGQDRSRILEPGMVLTVEPGLYIAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mimsiqnempgynemnoyinoogggclfpaemhglisgmicggnd
DSSWLPLihdlinegmarghelaqalrkmhsatsdalqddgrlfqlylpdgddvsyfd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MSVIIVGGGMAGATLALAISRLSHGALPVHLIEATAPESHAHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mSAQPVDIQIFGRSLRVNCPPDQRDALNQAADDLNQRLQDLKER
TRVTNTEQLVFIAALNISYELAQEKAKTRDYAASMEQRIRMLQQTIEQALLEQGRITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQNSDFWYFTGFNEPBAVLVLIKSDDTĤNHSVLFNRVRDLTAEIWFGRRLGQDAAPEK
LGVDRALAFSEINQQLYQLLNGLDVVYHAQGEYAYADVIVNSALEKLRKGSRQNLTAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(7749. .9599)
/note="similar to GenBank Accession Number D00398
(ECOAPP2)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="ORF_f441; third start codon"
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                                                                                                                                                                                                                                                                                                                                                                        14247 TCTCACAGGGCATTAAGCAACTGGAAAATATGTTCGGGCAGCCGCTGTTGGTGCGTACCG 14306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14307 TACCGCCGCCCCGACGGAACAAGGGCAAAAACTGCTGGCACTGCTGCCGCCAGGTGGAGT 14366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14547 TGCGCCGCGCGAAGTGGTCGCGCGGGGGAATTCAACATCAGGCGCTGCCGAGTTGTC 14606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgcggcgtggagatgttttaggagcggtaacccgtgaagctaatcccgtggcgggatgtg 454
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                                                                                                                                                                                                                                   35 tcattgatgaaggcagcttcgaaggcgcctccttagccctttccatttcccctcggcgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tgctgcaagcagaaactaaagcgcaactatctggacgccttgctgaaatcccgttaacca
                                                                   to GenBank Accession Number X01238
                                                                                                                                     Length 141744;
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                                                                                                                                       Score 82.6; DB 2; I
Pred. No. 1.4e-12;
0; Mismatches 234;
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10374. .10556
/gene="ssr"
10374. .10557
/note="similar t
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S. venezuelae pik
S. venezuelae pik
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Corynebacterium gl
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	` `	×	coryr	corynebacterium grutamiteum	T6 iimT	ncamica	<u>.</u>
	20: /cgn1_9/gcgdata/geneseq/geneseqn/NA1999.DAT:*	KW	Coryr	Corynebacterium glutamicum;	ium gl	utamicu	;;
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	22: /cgn1_9/gcgdata/geneseq/geneseqn/NA2001.DAT:*	KW	iduou	nonproteinogenic amino acid; linid: saturated fattu acid:	enic a	mino aci	ם כ
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Human low adenosin Human adenosine re Corn raffinose syn Human low adenosin

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Corynebacterium ql	DNA encoding Lysg,	BCG deletion regio	Genomic fragment #	Stealth virus nucl	Rice raffinose syn	Sequence of BamHI	P. aeruginosa tfdA	N. meningitidis pa	Neisseria meningit	S. venezuelae macr
DI	AAF71777	AAT96816	AAT33536	AAF28535	AAX84317	AAD00334	AAN80093	AAQ97857	AAA81464	AAF21609	AAZ87299
DB	22	18	17	22	20	21	6	16	21	21	21
Query Match Length DB ID	993	2374	15239	45613	4915	2842	2058	2058	102634	349980	4689
Query Match	100.0				5.2	4.8	4.2	4.2	4.2	4.2	4.0
Score	873	873	122.6	45.4	45.2	41.6	37	37	36.8	36.8	35
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RESULT AAF71777 ID AAF7 AAF71777 AAF71777 AAF71777 AXX AXX AXX AXX AXX CON CON CON CON CON CON CON C
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AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids from Corynebacterium glutamicum encoding metabolic · pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 G; 236 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microorganisms, useful for producing fin
microorganisms, including organic acids,
and purine and pyrimidine bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 226-228; 1737pp; English.
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                           99DE-1031457.
99DE-1031465.
99DE-1031478.
99DE-1031510.
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99DE-1031634.
99DE-1031636.
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                 0;
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  Length
                  Indels
Score 873; DB 22;
Pred. No. 1.9e-268;
Mismatches 0;
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100.0%;
Similarity 100.0%;
73; Conservative 0
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                                774 GAAGTCCTTGTGCAAGCAGCGCGGAAAATGGTGTTGCTGCAAGCAGAAACTAAAGCGCAA
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3382..14071
/note= "BCG delta 1 deletion region"
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                                               LySG; LySE; ORF3; lysine transport; regulatory protein; export protein; Microbial production; amino acid; animal feed additive; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This DNA, isolated from Corynebacterium glutamicum, contains the LysG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gcctccttagccctttccatttccccctcggcggtgagtcagcgcgttaaagctctcgag 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atgaaccccattcaactggacactttgctctcaatcattgatgaaggcagcttcgaaggc
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               encoding LysG, LysE and ORF3 from Corynebacterium glutamicum.
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                                                                                                                                 Location/Qualifiers
complement (82..954)
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/label= LysG
1016..1726
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/label= orf3
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                                                                                                  Corynebacterium glutamicum.
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                                                                                                                                                                                                                 This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdelta2. A specific genetic deletion of this region results in an avirulence phenotype of the mycobacterium. 2 Other deletion regions (see AAT33535 and AAT3357) have also been detected. Identification involved screening a BCG cosmid library with a radiolabeled probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H37Rv and avirulent BCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72
                                                                                                                                                                                                                                                                                                               The deletions provide useful markers for the identification of an avirulent, or a virulent, mycobacterial phenotype. Determination of avirulence requires the detection of the presence or absence of the deletion; the deletions are detected either by detecting the presence or absense of deletion junctions (see AAT3338-46), or by detecting the presence or absence or absence of the sequences contained within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5313 ctacatgicaccccitogoigticagicagogateaagicgitggagcaggaggegg
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                                                                                                                                   Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caagcagcgggaaaatggtgttgctgcaagcagaaactaaagcgcaactatctgg--ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gccttgctgaa----atcccgttaaccatcgccatcaacgcagattcgctatccacatgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gaagatgaagcgcacacattatccttgctgcggcgtggagatgttttaggagcggtaacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cgtgaagctaatcccgtggcgggatgtgaagtagtagaacttggaaccatgcgccacttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17; Length 15239;
                                                                                                                                                                                                                                                                                                                                                                                               Deletion polypeptides are used as components of
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15239 BP; 2878 A; 4791 C; 4729 G; 2841 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.0%; Score 122.6; DB 17; Length ilarity 49.9%; Pred. No. 1.7e-28; Conservative 0; Mismatches 409; Indels
                                                                                                                                                                                                                                                                                                                                                                                              the deletion. Deletion polypeptides immunological assays and in vaccines.
                                                                                                                                                                                          Example 1; Fig 2; 66pp; English
                           95us-0390878
 96WO-US01938
                                                    (PATH-) PATHOGENESIS CORP.
                                                                               Stover CK;
                                                                                                         WPI; 1996-393419/39.
                                                                                                                                                               bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 426; Conserv
                                                                              Mahairas GG,
15-FEB-1996;
                           17-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
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The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAR78834-AAR28854). The library has a number of uses described in the specification e.g. is useful for adentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis and meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic library; bacteria; human upper airway; otitis media; sinusitis;
                                                                                                                                                                                                          5903
                                                                                                                                                                                                                                                                                                                                                               5963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5844 egtaaggeetttegtegegeeateaceagaeegaegeaetttgteeegaeeaagaggge
                                                                                                                                                                                                                                                                                                                                                               5904 ttcaccgccgcagcgcgcgcgggctgggatggggcatgttccccgagaagctggcagca
                                                                                                                                                                                                                                                                                                                                                                                                                                           cccatgctaaaagcaggagaagtgatcctcctcgatgagatacccattgacacaccgatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5964 tetecgettgecgatggatcgttcgtacgggtctgcgacatacacetcgacgtccctete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gegatgecegtettaegetteggteecaaagatgtgetteaagaeegtgaeetggaeggg
                                                                geggetaaagetecgteactggegtggaategtgacgatggegtgcaggacatgttggtg
                                                                                                                                         cg---cgtcgatggtcctgtgggggggggggggggtatccattgtcccgtcggcggaaggt
                                                                                                                                                                                                                                                                                          tttggtgaggcaattcgccgaggccttggttggggacttcttcccgaaacccaagctgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bronchopulmonary; endocarditis; meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 180-191; 545pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berg KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF28535 standard; DNA; 45613 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUN-2000; 2000WO-US16649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0140121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6084 gcggcggcaagcg 6096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gatgcagcaatcg 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic fragment #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-041427/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200078968-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lagace RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF28535;
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Length 4915;

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AAD00334;
Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
AAD00334/c
                                                                                                                                                                                                            141
                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a Stealth virus nucleic acid clone. The invention relates to a method of detecting and characterising a stealth virus by reacting a sample suspected of containing a stealth virus with a probe from a known stealth virus and sequencing the resultant isolated nucleotide. The method comprises the steps of: (a) isolating DNA or RNA croma sample suspected of containing a stealth virus, e.g. a culture of cells showing a viral cytopathic effect; (b) testing the reactivity of the isolated DNA or RNA with a molecular probe that contains at least 18 or more contiguous nucleotides identical to sequence previously identified from a stealth virus; and, optionally (c) sequencing the isolated DNA or RNA molecules that react with the probe. The method is solated DNA or RNA molecules that react with the probe. The method is used to detect stealth virus in a biological product, food or in the convironment. The method is also used to evaluate agents for their inhibitory or stimulatory effects on stealth virus replication and to determine capacity of the virus to recombine with and potentially alter the nucleic acid sequences of a cell or bacterium.
                                                                                                      ö
                                                                                                                                                                        10609 ATGAATACCACAAATCTTGCCACTTTTGTTGCAGTTATGCAGACAGGCAGCATCTCTAGT 10550
                                                                                                                                                                                                                                          61 gectecttagecettteeattteeeeteggeggtgagtcageggttaaagetetegag 120
                                                                                                        Gaps
                                                                                                                                     1 atgaaccccattcaactggacactttgctctcaatcattgatgaaggcagcttcgaaggc 60
                                                                  Length 45613;
                                                                                                     ;
                Sequence 45613 BP; 13249 A; 9346 C; 9947 G; 13071 T; 0 other;
                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4915 BP; 967 A; 1521 C; 1591 G; 828 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stealth virus; detection; diagnosis; infection; ss.
                                                                  Score 45.4; DB 22;
Pred. No. 0.0012;
); Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 19; Page 40-42; 95pp; English.
                                                                                                                                                                                                                                                                                                             10489 GATGAATTTGGGACGGCGTTGTT 10467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stealth virus nucleic acid clone,
                                                                                                                                                                                                                                                                             121 catcacgtgggtcgagtgttggt 143.
                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel strains of stealth virus
                                                                                                                                                                                                                                                                                                                                                                                                AAX84317 standard; DNA; 4915
                                                                  57.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US27744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0001184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                     82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-405521/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MART/) MARTIN W J.
                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stealth virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9934019-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Martin WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX84317;
                                                                    Query Match
                                                                                   Best Local
                                                                                                                                                                                                                                                                                                                                                                                AAX84317/c
                                                                                                   Matches
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The present sequence is a cDNA encoding raffinose synthase from clone rls72.pk0020.d9 isolated from a rice infected leaf CDNA library rls72. Raffinose synthase is involved in the blosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids and encoded proteins involved in the biosynthesis of raffinose, useful for producing soybean seeds with a reduced raffinose content and therefore improved nutritional quality -
                                                                                                   1461 CACTCTTGCTGCTGTTGCTGACGCAGGATCTCTCGACGGTGCAGCGCATGAACTCCGCAT 1402
                                                                                                                                                                   1401 TACTCCCTCCGCTGTGAGCCAGCGCTCAAGGCTTTGGAGACTCTTCTTGGTCAGGTCGT 1342
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                    ggtatcgcgcacccaaccggccaaagcaaccgaagcgggtgaagtccttgtgcaagcagc
                                                                     cactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagccctttccat
                                                                                                                                    ttececeteggeggtgagteagegegttaaagetetegageateaegtggggtegagtgtt
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice; raffinose synthase; raffinose saccharide; soybean; clone rls72.pk0020.d9; nutritional; soy protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rice raffinose synthase cDNA from clone rls72.pk0020.d9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2842 BP; 520 A; 887 C; 954 G; 481 T; 0 other;
Score 45.2; DB 20;
Pred. No. 0.0005;
0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag* a
/product= "Raffinose synthase"
                                                                                                                                                                                                                                                                                           201 gcggaaaatggtgttgctgcaagcagaaac 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
215..2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 42-43; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                       AAD00334 standard; cDNA; 2842
 5.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-350754/30.
P-PSDB; AAY70977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allen SM, Hitz WD;
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200024915-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAY-2000.
                                    107;
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Sequence 2058 BP; 372 A; 659 C; 661 G; 366 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaphammer BJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1994;
11-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9518862-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUL-1995
                                                                                                                                                                                                                                                                                                                    AAQ97857;
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                                                 625 gggcgcaggcgcgtatccattgtcccgtcggcggaaggttttggtgaggcaattcgccga 684
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                Sequence of BamHI/SalI fragment of the tfdA gene which encodes 2,4-dichlorophenoxyacetic acid (2,4-D) mono-oxygenase.
                                                                                                                                                         685 ggccttggttggggacttcttcccgaaacccaagctgctcccatgctaaaagcaggagaa
                                                                                                                               922 GCGCGGCGCGCCCCCATTGGCGAGGCTGCGGAGGCCCTGCTTGACGCCGTCGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmids and bacteria contg. gene tfdA for 2,4\text{-}D\text{-}mono:oxygenase} isolated using new Alcaligenes eutrophus transposon mutants
                           .;
0
Length 2842;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        resistance; halogenated aromatic cpd; enzyme;
 Score 41.6; DB 21;
Pred. No. 0.0054;
               Pred. No. 0.00
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
748..1608
/*tag= a
/note= "DNA SQ claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 10; 32pp; German.
                                                                                                                                                                                                                                                                                       AAN80093/c
ID AAN80093 standard; DNA; 2058 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zenk M;
                                                                                                                                                                                                               745 gtgatcctcctcgatgagat 764
                                                                                                                                                                                                                                      802 CITCITCITGICCCIGIGGI 783
 4.8%;
50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alcaligenes eutrophus JMP134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86DE-3629890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86DE-3629890
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SCHD ) SCHERING AG.
(STRE/) STREBER W R.
(MACQ-) MACQUARIE UNIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streber W, Timmis KN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1988-071716/11.
P-PSDB; AAP80079.
                                                                                                                                                                                                                                                                                                                                                                                                                                     mono-oxygenase; ss.
            Local Similarity
ses 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                        30-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE3629890-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                     Herbicide
                                                                                                                                                                                                                                                                                                                              AAN80093;
 Query Match
                        Matches
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Gaps
                                                                                 13 caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Using presence of tfdA gene to select transgenic plants - imparting resistance to 2,4-di:chloro:phenoxy:acetic acid, esp. sweetgum (Liquidamber) trees contg. this gene and plantations of them
                                                                                                                                                                                                                                                                                                                                                                     Transgenic plant; tfdA gene; 2,4-dichlorophenoxyacetic acid; 2,4-D; herbicide resistance; sweetgum; Liquidamber styraciflua; hardwood; plantation; crop improvement; selectable marker; pUCW200; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A tidA gene of P. aeruginosa plasmid pRO101, which encodes the enzymes for 2,4-D degradation, was cloned into Agrobacterium tumefaciens vector pB1121 to form pUCW200. This was used to introduce 2,4-D herbicide-resistance into sweetgum, thereby allowing selection of transgenic plants and reducing the cost of
                            ;
0
Length 2058;
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2058 BP; 372 A; 659 C; 661 G; 366 T; 0 other;
                            65;
DB 9;
0.14;
                            Mismatches
Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
751..1611
/*tag= a
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                                                                                                                                                                                                                                                              ВР
                            0;
                                                                                                                                                                  133 cgagtgttggtatcgcgcacc 153
                                                                                                                                                                                           410 GTGTTGTTGTTCGAGCGCAGC 390
                                                                                                                                                                                                                                                             AAQ97857 standard; DNA; 2058
 4.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0358117.
94US-0179667.
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                                                                                                                                                                                                                                                                                                                   (first entry)
Query Match
Best Local Similarity 53.99
Matches 76; Conservative

 P. aeruginosa tfdA gene.

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                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
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P-PSDB; AAR79659.
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proteins from Neisseria genomic sequences. AAAB1453 to AAAB2414.

Corporating from Neisseria genomic sequences. AAAB1453 to AAB2414.

Corposent specifically claimed Neisseria meningitidis genomic DNA sequences; AAAB1201 to AAAB25601 to AAB2563 represent. AAAB1254 to AAAB1259 and AAAB1304 to AAAB1321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAAB1322 to AAAB1452 represent Neisseria meningitidis Menb polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition on the used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neisseriae. Identification of sequences from the bacterium will also facilitate production of blological probes,
                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
                                                                                                                                              73 ctttccatttcccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt 132
                                                                                                                                                                 Gaps
                                                                        caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention describes methods of obtaining immunogenic
                                      .;
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Score 37; DB 16; Length 2058;
Pred. No. 0.14;
); Mismatches 65; Indels
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Ratti G, Scarselli M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     N. meningitidis partial DNA sequence gnm_12 SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 353-383; 1760pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Masignani V, Galeotti C, Mora M, Rappuoli R, Pizza M;
                                                                                                                                                                                                                                                                                                                                           AAA81464 standard; DNA; 102634 BP.
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0
                                                                                                                                                                                                                                                    410 GTGTTGTTGTTCGAGCGCAGC 390
                                                                                                                                                                                                               133 cgagtgttggtatcgcgcacc 153
 4.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-318079/27.
                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  04-DEC-2000
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   Query Match
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                    Best Loca
Matches
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particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions.
                                                                                                                                                                                                                                                                                                                                                                                                  Masignani V;
Rappuoli R;
                                                                                                                                                                                                                                                                                                                                           62462 atggatgccgtacaattaaaatcatttgtcgccgtcgcgcacgagggcaaccttacccaa 62521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21634 and AAF21607 to AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                gcctccttagccctttccatttccccctcggcggtgagtcagcgcgttaaagctctcgag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections \cdot
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                       1 atgaaccccattcaactggacactttgctctcaatcattgatgaaggcagcttcgaaggc 60
                                                                                                                                                                     Sequence 102634 BP; 23871 A; 24828 C; 27888 G; 26042 T; 5 other;
                                                                                                                                                                                                                               21; Length 102634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis B nucleotide sequence SEQ ID NO:110.
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Scarlato V,
                                                                                                                                                                                                                                                                72; Indels
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Galeotti C, Mora M, Ratti G, Scarselli M, S
Frazer CM, Grandi G;
                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                             Score 36.8; DB Pred. No. 0.99; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62582 gaatatgtcggcacgccgctgttcaggcgcac 62613
                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 catcacgtgggtcgagtgttggtatcgcgcac 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Appendix A; 692pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF21609 standard; DNA; 349980 BP
                                                                                                                                                                                                                                 4.28;
52.68;
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99WO-US23573.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Best Local Similarity 52.6
Matches 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
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Desosamine and macrolide biosynthetic gene clusters, useful for, e

synthesis of methymycin and pikromycin Claim 15; Page 415-417; 438pp; English.

2000-160679/14

P-PSDB; AAY77194

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sequences which overlap each other at the beginning and end of each the beginning of AAP21607, the last 49980 bp of AAP21644 is repeated at the beginning of AAP21607, the last 49980 bp of AAP21607 are repeated at the beginning of AAP21608, and so on). AAP21655 to AAP21686 encode the Neisseria proteins given in AAB58550 to AAB58593, and AAP21889 to AAP21606 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. Neisserial nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial
                                                                                                                                                                                                                                                                                                                                                                                                bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently
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Sequence 349980 BP; 81351 A; 86755 C; 95584 G; 86290 T; 0 other;

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Db 166174 atggatgccgtacaattaaaatcatttgtcgccgtcgcgcacgagggcaaccttacccaa 166233
                                                                                              1 atgaaccccattcaactggacactttgctctcaatcattgatgaaggcagcttcgaaggc 60
    Length 349980;
  21;
    DB
Score 36.8; DE
Pred. No. 1.8;
0; Mismatches
Query Match
Best Local Similarity 52.6%;
Matches 80; Conservative
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Db 166234 gccgccaaacgacttttcctttcccagcctgccgtttctgcccaaattaaagcccttgaa 166293 61 gcctccttagccctttccatttcccctcggcggtgagtcagcgcgttaaagctctcgag 120 ò

Db 166294 gaatatgtcggcacgccgctgttcaggcgcac 166325 121 catcacgtgggtcgagtgttggtatcgcgcac 152 õ

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Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent; ds.
                                                                                          S. venezuelae macrolide biosynthetic gene pikAIII, SEQ ID NO:34.
                                                                                                                                                                                        Streptomyces venezuelae ATCC15439.
                    AAZ87299 standard; DNA; 4689 BP
                                                                   05-JUN-2000 (first entry)
                                          AAZ87299;
RESULT 11
           AAZ87299/
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Location/Qualifiers 1..4689 /*tag= a /product= "PikAIII" 99WO-US14398 WO200000620-A2 25-JUN-1999; 06-JAN-2000

Liu H, Xue Y, Zhao L;

Sherman DH,

98US-0105537

26-JUN-1998;

(MINU) UNIV MINNESOTA.

production of blologically active macrolides. The macrolide blosynthetic production of blologically active macrolides. The macrolide blosynthetic proteins are useful for synthesis of methymycin, pikromycin, of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryc gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, pixromycin, neomethymycin, natomorphiant or augmented cells compoination of these compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the 2811 ccacceccesacasercescrescesses as a second contract contraction of the contract 2991 GAGGTCGTCGAGGAGCGAGACCACGCCGGTGAAGCCGTCGCCGGTCGTCAGTGCGGTGAG 2932 as viral parasitic pathogens, or as crop protection agents (e.g., fundicides or insecticides) via expression of polyfetides in plants. Sequences AA&87295-287302 represent macrolide biosynthetic genes from Streptomyces venezuelae ATCC 15439, which encode proteins 406 gatgttttaggagcggtaacccgtgaagctaatcccgtggcgggatgtgaagtagtagaa 465 466 cttggaaccatgcgccacttggccattgcaaccccctcattgcgggatgcctacatggtt 525 526 gatgggaaactagattgggctgcgatgcccgtcttacgcttcggtcccaaagatgtgctt 2931 CCGGGCGGCGAGGCCTCACGGTCGTCGTCGCCCCGGCTTCCAGTACGTCGACCTCCGC caagaccgtgaccgggcgcgtcgatggtcctgtggggcgcaggcgcgtatccatt Score 35; DB 21; Length 4689; Pred. No. 0.87; 0; Mismatches 145; Indels Sequence 4689 BP; 648 A; 1882 C; 1572 G; 587 T; 0 other; 2751 ACGCCAGTCGTCGCGCGCGTGGG 2725 646 gtcccgtcggcggaaggttttggtgag 672 AAZ87318/c ID AAZ87318 standard; DNA; 36778 BP 4.08; 45.78; 05-JUN-2000 (first entry) Matches 122; Conservative Query Match Best Local Similarity AAY77190-Y77197 AAZ87318; 286 QQ δ δ qq Ω g

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Length 36778;

gatgttttaggagcggtaacccgtgaagctaatcccgtggcggggatgtgaagtagtagaa 465

0; Mismatches 145; Indels

Score 35; DB 21; Pred. No. 2.3;

4.08;

Matches 122; Conservative

406

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466

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Similarity

Query Match Best Local

SSXS

biosynthetic gene cluster (pik) from Streptomyces venezuelae ATCC 15439, as given in figure 31.

Sequence 36778 BP; 4758 A; 14303 C; 12864 G; 4851 T; 2 other;

29921 CCGGGCGGCGAGGGCCTCACGGTCGTCGTCGCCCGGCTTCCAGTACGTCGACCTCCGC 29862

cttggaaccatgcccacttggccattgcaaccccctcattgcgggatgcctacatggtt

gatgggaaactagattgggctgcgatgcccgtcttacgcttcggtcccaaagatgtgctt

29801 CCACCGCCGGACAGGTCCGCCTGGCCGGAGGCCGTCAGCGGCTTCCACTCGACGCGGTA 29742

BP

AA287285 standard; DNA; 37948

AAZ87285/

(first entry)

05-JUN-2000

AAZ87285;

caagaccgtgacctggacggcgtcgatggtcctgtggggcgcaggcgcgtatccatt

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Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent; ds.
                                                                                                                                                                                                                                                                          /product= "Pik gene cluster protein #1 (AAY77200)"
15688..26907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'product= "Pik gene cluster protein #4 (AAY77203)"
                                                                                                                                                                                                                                                                                                                                              /product= "Pik gene cluster protein #2 (AAY77201)"
26991..31679
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Pik gene cluster protein #3 (AAY77202)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Pik gene cluster protein #4 (AAY80997)"
S. venezuelae pik (macrolide biosynthesis) gene cluster.
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                                                                                                                                                                                                                            Location/Qualifiers
1742..15583
                                                                                                                                                                                 Streptomyces venezuelae ATCC15439
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Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemocherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desosamine and macrolide biosynthetic gene clusters, useful for, e .g.
                                                                                                               venezuelae pik (macrolide biosynthesis) gene cluster, SEQ ID NO:5.
                                                                                                                                                                                                                                                                                            hypercholesterolaemia; crop protection agent; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 299-315; 438pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthesis of methymycin and pikromycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao L;
                                                                                                                                                                                                                                                                                                                                                 Streptomyces venezuelae ATCC15439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JAN-2000.
comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryc gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, parbomycin, narbomycin, or augmented cells combination of these compounds. Recombinant or augmented cells comprising the desosamine compounds. Recombinant or augmented cells comprising the desosamine of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, pixromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           such as chemotherapeutics, immunosuppressants, agents to treat asthma, cretonic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. The present sequence represents the macrolide
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and/or macrolide blosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide blosynthetic proteins are useful for synthetic gene clusters are useful for the production of biologically active macrolides. The macrolide blosynthetic proteins are useful for synthesis of methywycin, pikromycin, neomethywycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) of monomers. The compounds produced by the recombinant host cells are useful as blopolymers, e.g., in packaging or biomedical applications, to so hopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of coganisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., funglicides or insecticides) via expression of polyketides in plants. The present sequence represents the macrolide biosynthetic gene cluster (pik) from Streptomyces venezuelae ATCC 15439.
Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, pikromycin, neomethymycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosamine
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; 0 31031 TCCCGCGGCCTTCAGCGCCCCAGCAGCTCGGCTTCTGGCTCCGCTCCCGACGGCGACGACGAT 30972 30971 CCACCGCCGGACAGGTCCGCCTGGCCGGAGGCCGTCAGCGGCTTCCACTCGACGCGGGTA 30912 31151 GAGGTCGTCGAGGAGCGAGACCACGCCGGTGAAGCCGTCGTCGCTCGTCGTGCGGTGAG 31092 31091 CCGGGCGGCGAGGGCCTCACGGTCGTCGTCGCCCCGGCTTCCAGTACGTCGACCTCGC 31032 406 gatgitttaggagcggtaacccgtgaagctaatcccgtggcgggatgtgaagtagtagaa 465 466 cttggaaccatgcgccacttggccattgcaaccccttattgcgggatgcctacatggtt 525 Gaps 526 gatgggaaactagattgggctgcgatgcccgtcttacgcttcggtcccaaagatgtgctt 0; DB 21; Length 37948; Score 35; DB 21; Length 37 Pred. No. 2.3; 0; Mismatches 145; Indels 30911 ACGCCAGTCGTCGCCGCGCTGGTGGG 30885 646 gtcccgtcggcggaaggttttggtgag 672 4.0%; Query Match Best Local Similarity 45.73 Matches 122, Conservative g g g g ð g ð ò ò

for every an antibiotics and as intermediates in the synthesis of compounds with pharmaceutical value. The DNA compounds may also encode a C12-hydroxyalse (picK), desosamine biosynthesis and desosaminyl transferase enzymes (useful for conversion of ketolides to antibiotics), and the beta-glucosidase enzyme (involved in picromycin biosynthesis). These compounds are also useful for increasing the antibiotic activity

of a compound relative to the unhydroxylated compound. The recombinant host cells are useful as genetic systems that allow rapid engineering of the narbonolide polyketide synthase. These would be valuable for creating novel ketolide analogs for pharmaceutical applications.

of the invention. The specification describes a recombinant DNA compound expressing recombinant polyketide synthase genes in host cells for the production of narbonolide, narbonolide derivatives and polyketides that

The present sequence is used to produce the recombinant DNA compounds

Disclosure; Columns 15-32; 117pp; English.

New recombinant pick hydroxylase gene of Streptomyces venezuelae useful for converting ketolides to antibiotics and as antibiotics and intermediates in the synthesis of compounds with pharmaceutical value

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McDaniel

Tang L,

Betlach M,

Betlach MC,

Ashley G,

WPI; 2000-610844/58

BIOSCIENCES INC.

(KOSA-) KOSAN

98US-0100880. 98US-0100880. 99US-0119139. 99US-0134990 97US-0846247 98US-0073538 98US-0141908

28-MAY-1998; 22-SEP-1998; 08-FEB-1999; 20-MAY-1999 06-MAY-1998; 28-AUG-1998 30-APR-1997

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Narbonolide synthase; polyketide synthase gene; narbonolide polyketide;
                                                                                                                                    antibiotic; C12-hydroxyalse; picK; desosamine biosynthesis; desosaminyl transferase enzyme; ketolide; beta-glucosidase enzyme;
                                                                                               Nucleotide sequence of the insert DNA in cosmid pKOS023-27.
                     AAA75633 standard; DNA; 38506
                                                                                                                                                          picromycin biosynthesis; ss
                                                                      (first entry)
                                                                                                                                                                                    Streptomyces venezuelae
                                                                        22-JAN-2001
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                                               AAA75633;
RESULT 14
          AAA75633,
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99US-0320878.

27-MAY-1999;

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Matches 122; Conservative
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ID AAZ56001 standard;
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This is the recombinant cosmid pKOSO23-27 DNA sequence which contains a Streptomyces venezuelae DNA insert. The cosmid contains open reading frames which encode the various modules of the narbonolide polyketide synthase (PKS). The invention relates to recombinant DNA containing a coding sequence for a narbonolide PKS. Polyketides are compounds synthesized from 2-carbon units through a series of condensations and subsequent modifications. Modular PKSs are responsible for the production of many antibiotics including picromycin. The narbonolide PKS consists of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAY67201, AAY67202, AAY67203, AAY67204, AAY67205, AAY67207
AAY67208, AAY67211.
                          Narbonolide polyketide synthase; PKS; cosmid pKOS023-27; ketolide;
antibiotic production; narbomycin; picromycin; ds.
Recombinant cosmid pKOS023-27 containing S. venezuelae PKS genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA encoding a domain of narbonolide polyketide synthase, for production of ketolide antibiotics -
                                                                                                                                                                                                                                                                                                                                        "Contains typeII thioesterase domain"
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                                                                                                                                                                                                                                                                                                                                                                                   /note= "4-keto-6-deoxyglucose isomerase"
36159..37439
                                                                                                                                        synthase subunit 1"
                                                                                                                                                                                  /note= "Narbonolide synthase subunit
25133..29821
                                                                                                                                                                                                                             note= "Narbonolide synthase subunit
29924..33964
                                                                                                                                                                                                                                                                                        note= "Narbonolide synthase subunit
13961..34806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "3-amino dimethyltransferase'
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37529..38242
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                                                                                                                                       'note= "Narbonolide
3830..25049
                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                              /product= PICCIII
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98US-0141908.
98US-0100880.
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/*tag= a
                                                              Streptomyces venezuelae.
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proteins make up the narbonolide PKS (PICAI, PICAII, PICAII and PICAIV). PICAII includes the loading module and extender modules 1 and 2, PICAII includes extender modules 3 and 4, PICAIII includes extender module 5 and recludes extender module 5 and 2. PICAII includes extender module 5 and PICAIV includes extender module 6 and a type II thioesterase domain. The second type II thioesterase domain is found on the PICB protein. The nucleotide sequences encoding all of these proteins can be isolated in recombinant form from the recombinant cosmid pKOSO13-27. Narbonolide is classease and is required for this conversion, and the desosamine biosynthetic genes are also found in cosmid pKOSO13-27. The recombinant DNA of the invention is used to express, in transformed cells, narbonolide (or its derivatives) or other ketolides (particularly narbonolide (or its derivatives) or other ketolides (particularly recombinantly expressed in the same hosts) to polyketide antibiotics or their intermediates. The antibiotics are useful in human or veterinary
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/note="Wetcor: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) http://www.edgp.ebi.ac.uk · This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                    Tel: (206) 616-3818

Tex: (206) 616-3887

Email: jwallacetu.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC clones are derived from the human BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu.clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSO17SY 1101 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46; Indels
                                                          High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40.6; DB 228;
Pred. No. 0.21;
0; Mismatches 46;
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                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                             Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                            High quality sequence stop: 436.
Location/Qualifiers
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Best Local Similarity 59.3
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                         .436
                                                                                                                                                                                                                                                              Seq primer: SP6
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JOURNAL
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AI513856 GH26967.5
BE978396 bs78c03.y
AI109136 GH08244.5
AI947010 bs34a07.y
AI513839 GH26960.5
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A1674676 wd19b03.x
A1928356 w096c11.x
A1123743 oo21b12.x
                                                                                                                                                                                  AQ851405 LMAJFV1_1
AZ135253 OSJNBD011
AZ127284 OSJNBD008
BE605012 WHE1713-1
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BF490406 AT26864.5
A1389466 GH20646.5
A1337304 tb98a08.x
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OSJNBB011
OSJNBB008
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602294752
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AT19875.5
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BE977760 DS68904.Y
BF500739 AT15754.5
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 436)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                      R21101 y952h08.rl
AA461278 zx63c04.r
BF031515 601559336
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AW327833 dr02f02.x
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BF194891 7089h11.x
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AV627993 AV627993
AV629482 AV629482
AV641278 AV641278
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AL053013 I
BF503196 P
BE387930 G
BF485823 P
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BG027707
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AW327833
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d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genome survey sequence TET3 end of BAC # BACK19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL053013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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1 (bases 1 to 925)
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14.4%; Pred. No. 0.
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/organism="Drosophila me/plasmid="paeloBAC11"
/db_xref="taxon:7227"
/clone_lib="brosBAC"
/clone="BACN37L08"
                                                                                                                                                   Location/Qualifiers
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Direct Submission
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Stapleton, M., Broksteln, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Change, M., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Park, S., Pargass, V., Phouanenavong, S., Wan, K., Yu, C., Lewis, S. E., Berkeley, Drosophila Gene Collection Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó,
NY. The library is named RPCI-98 and was constructed by partial. BECORI digestion of Drosophila DNA provided by the BDCP from the isogenic strain y2; cn bw sp, the same strain used for the BDCP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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AT19123.9prime AT Drosophila melanogaster adult testes POTB7
Drosophila melanogaster CDNA clone AT19123 5 similar to CG17137:
FBan0017137 last_updated:000321, mRNA sequence.
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Bukaryota: Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 667)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
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                                                                                                                                                                                                                                                                                                                                                                                                               DB 219;
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ilarity 15.0%; Pred. No. 2.1;
Conservative 130; Mismatches 142;
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BDGP
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Best Local Similarity
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Lawrence Berkeley National Lab

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/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
CORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
a 171 c 269 g 172 t
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Eukaryota: Metazoa; Arthropoda: Tracheata: Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota: Diptera: Brachycera;
Muscomorpha: Ephydroidea: Drosophilidae; Drosophila.

[ (bases 1 to 650)
1 (bases 1 to 650)
2 (bayaroidea, Drosophilidae; Drosophila.

B. Carlson,J., Champe,M., Chavez,C., Chew,M., Dorsett,V., Farfan,D., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P.,
Lido,G., Miranda,A., Misra,S., Mungall,C.J., Nunco,J., Pacleb,J.,
Park,S., Paragas,V., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E.,
Celniker,S. and Rubin,G.M.
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/clone_lib="AT Drosophila melanogaster adult testes pOTB7"
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AR19875.5prime AT Drosophila melanogaster adult testes pOTB7
Drosophila melanogaster CDNA clone AT19875 5 similar to CG13768:
FBan0013768 last_updated:000321, mRNA sequence.
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//lab_host="Plates AT.10.AT.120: DH5-alpha. Plates
AT.121-AT.319: DH5-alpha TonA"
//note="Organ: ADULT testes; Vector: pOTB7; Site_1: EcoR Site_2: Xho1; The mRNA for the testis library was made
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AE003614
Plate: AT.198 row: G column: 3
High quality sequence stop: 633.
Location/Qualifiers
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                       DB 167;
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Pred. No. 6.2;
0; Mismatches
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                                                        /clone_lib="NIH_MGC_44"
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                                                                                                                                                                                                                                                                                                                                                                                                                    4.18;
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                                                                                                                                                                                                                                                                                                            /sex="mails" // (Adv. stages="0-3" day old Ore-R mailss" // (Adv. stages="0-3" day old Ore-R mailss" // (Adv. stages="0-3" day old Ore-R mailss" // (Adv. stages="0-3" day old Ore-R mailss // (Ante-"Organ: ADULT testes: Vector: pOTB7; Site_1: ECORI; Site_2: Ahol; The mRNA for the testis library was made from testes and seminal vessicles hand dissected from 0-3 day old Ore-R mailss. RNA kindly provided by the lab of Margaret Fuller. Sized fractionated cDNAs were directly ligated into porB7. Plasmid CDNA library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 785)
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 149; Length 667;
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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                                                                             hit genomic sequence AE003630
Plate: AT.191 row: B column: 11
High quality sequence stop: 545.
Location/Qualifiers
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Location/Qualifiers
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Tissue Procurement: ATCC
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Best Local Similarity 52.77
Matches 78; Conservative
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BE387930
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Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.
Seq primer: -40RP from Gibco
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from testes and seminal vessicles hand dissected from 0-3 day old Ore-R males. RNA kindly provided by the lab of Margaret Fuller. Sized fractionated cDNAs were directly ligated into porpr. plasmid cDNA library."
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/clone="LMA_FV1_Im40b11"
/clone="LMA_FV1_Im40b11"
/clone="Lib="Le1shmania major FV1 random genomic library"
/lab_host="T00P10 (Invitrogen)"
/note="vector: pZero-2 (Invitrogen); Site_1: EcoRV;
Genomic DNA was isolated from stationary phase cells. For
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Leishmania major genomic clone LMAJFV1_lm40b11 5', DNA seguence.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                            Length 650;
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                         DB 149;
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                                                                                                                                                                                                                       Score 35.8; DE
Pred. No. 6.8;
                                                                                                                                                                                                                    Query Match 4.1%; Score 35.8; D
Best Local Similarity 65.8%; Pred. No. 6.8;
Matches 52; Conservative 0; Mismatches
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Location/Qualifiers
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AQ851405.1 GI:6056053
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Anote—"Vector: DRACINGING:
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arunuqanathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline phosphatase and ligated into pZero-2 vector's EcoRV site."
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Rice BAC Library (EcoRI) Oryza sativa genomic
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                                                                                                                                                                                                                                                                                                                                                                                        245 ACTAGCAGTAATCGCAGCAGCGAAACCGGGAGGGATCGTGAAGACCTGGTTAGCCAGCAGCGAAAAC
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A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
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                                                                                                                                                                                       Length 393;
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/clone_lib="CUGI Rice BAC Library (EcoRI)"
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Clemson University Genomics Institute
                                                                                                                                                                                     Score 35.6; Di
Pred. No. 6.8;
0; Mismatches
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/lab_host="E. coli DH10B"
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Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GTAAAACGACGCCAGTG
Class: BAC ends
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High quality sequence stop: 590.
Location/Qualifiers
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/db_xref="taxon:4530"
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ilarity 53.6%;
Conservative
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Oryza sativa
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Matches 74; Conserv
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cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRi as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
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/note="Westor: pBACindigo: Site_1: EcoRI; Site_2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n-24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
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Rice BAC Library (EcoRI) Oryza sativa genomic
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/db_xref="taxon:4530"
/clone="0SNBbD0084306f"
/clone_lib="CuGI Rice BAC Library (EcoRI)"
/tissue_type="Leaf"
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Tel: 864 656 7288
Fax: 864 656 4293
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Pred. No. 7.8;
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OSJNBb0084J06f CUGI Rice BAC Librar
clone OSJNBb0084J06f, DNA sequence.
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/strain="Japonica"
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High quality sequence stop: 745.
Location/Qualiflers
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Seg primer: GTAAAACGACGGCCAGTG
Class: BAC ends
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Matches 65; Conscrete
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Oryza sativa
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AUTHORS
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Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximatley 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE605012 592 bp mRNA EST 21-AUG-2000 WHE1713-1716_A23_A232S Wheat heat stressed spike cDNA library Triticum aestivum cDNA clone WHE1713-1716_A23_A23, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     529 gggaaactagattgggctgcgatgcccgtcttacgcttcggtcccaaagatgtgcttcaa 588
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Strategene SK primer.
Location/Qualifiers
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/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Spikes at 5, 10, 15 and 20 days after
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800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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Pred. No. 8.3;
0; Mismatches
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/db_xref="taxon:4565"
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Matches 65; Conservative
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ORIGIN

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Site_1: ECORI; Site_2: XhoI; Spikes at 5, 10, 15 and 20 days after anthesis were heat stressed under two conditions at Texas Tech University (D. Zhang in HT Nguyrn lab): (1) at 38 C for 4 hours and (2) 5 days of cyclic treatment' of 38 C for 4 hours. Total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton, Malatrasi) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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/lab_host="E. coli strain XLOLR"
/lab_host="E. coli strain XLOLR"
/note="vector: pBk-CMY; Site_1: ECORI; Site_2: XhoI; This CDNA library was constructed from polya+ enriched mRNA from mycellum grown in liquid medium for 3 weeks at 25 c in the dark in a liquid synthetic medium of 2.4 g sucrose in the dark in a liquid synthetic medium of 2.4 g sucrose of the sparagine, 10 mg cholesterol, 10 mg assorbate,
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CQUtOb.D., Hraber.P.T., Sobral,B.W.S. and Gijzen,M.
Comparative analysis of expressed sequences in Phytophthora sojae Plant Physiol. 123 (1), 243-254 (2000)
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Phytophthora.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      525 tgatgggaaactagattgggctgcgatgcccgtcttacgcttcggtcccaaagatgtgct
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9-3E-MY PsojaeMY Phytophthora sojae CDNA, mRNA sequence.
BE582886
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1391 Sandford Street, London, Ontario, Canada NSV 4T3
Tel: 519 457 1470
Exx: 519 457 3997
Email: gljzenm@em.agr.ca.
Locaton/Qualifiers
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/strain="race 2, strain p6497"
/db_xref="taxon:67593"
/clone_lib="PsojaeMY"
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Pred. No. 8.8;
0; Mismatches
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Best Local Similarity 50.3%;
Matches 87; Conservative
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Phytophthora sojae
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Direct Submission

Ly Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

By 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://Decper.med.buffalo.edu/drosophila_bac.htm.
using E. coli host strain XL1 Blue MRF'. Inserts were then subcloned by mass excision using ExAssist helper phage for conversion into phagemid vector pBK-CMV in E. coli host strain XLOLR. Sequenced using T3 primer: 5' ATT AAC CCT CAC TPA AGG S4'." 96 t 2 others
                                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 CCACTAGGTCGTCCACGAGCAGCACGCGGTCGCCTTGTTGATGACGCGTACGCCTGGATGC 256
                                                                                                                                                                                                                                                                                                                                                                 434 CTTGATGGCGCGCGCGCGCGCTCCAGCACGCGGATCTCGACCACGAAGATGCAGGCCGT 375
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                            535 ctagattgggctgcgatgccgtcttacgcttcggtcccaaagatgtgcttcaagaccgt
                                                                                                                                                                                                                                                                                                                                                                                                                      gacctggacgggcgcgtcgatggtcctgtggggcgcaggcgcgtatccattgtcccgtcg
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR28N12"
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/clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
/fclone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
/fclone_lib="Chlamydomonas reinhardtis 51te_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"
140 c 126 g 67 t
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute 22-0812, Japan
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Chlamydomonas reinhardtii.
Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 424)
Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Nakamura,Y. and Tabata,S.
Generation of expressed sequence tags from low-CO2 and high-CO2
DNA Res. 7 (5), 305-307 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                    5% to 0.04% CO2 Chlamydomonas 5', mRNA sequence.
                                                                                                         cttggccattgcaacccctcattgcgggatgcctacatggttgatgggaaactagattg 542
                                                                                                                         614 MRCSTMWHWKMKXGTINCWDMGTCMABGMHAWVGTACBWBCRYDTGGTSAGTSAYMTCYV 555
                                                                                                                                                                                                                                               554 HKCGTGTKSCGCGWGDCGYKYTGRKCWBHMSGAVCKMMGCSBTGYTGYMTCGVGNGSKCG 495
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    .424
/organism="Chlamydomonas reinhardtii"

                                          DB 219;
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                                                           ; Pred. No. 12;
85; Mismatches
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reinhardtii CDNA clone LCL090h04_r
AV631247
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/db_xref="taxon:3055"
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Matches 87;
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/clone_lto_rto_ssilo_rto_ssilo_rto_ssilo_rto_rto_rto_ssilo_rto_rto_ssilo_rto_rto_ssilo_rto_ssilo_rto_rto_ssilo_rto_ssilo_rto_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_rto_ssilo_
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
LocatLoh/Qualifiers
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Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Nakamura,Y. and Tabata,S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV627993 437 bp mRNA EST 15-DEC-2000 AV627993 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas reinhardtii cDNA clone LCL035a10_r 5', mRNA sequence.
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152 CTGCGAGAACTTCTCGAAGCCGCCCTCTTGTTCTGAAACTTCTTGAA
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                                                                                                                                                                      ctagattgggctgcgatgcccgtcttacgcttcggtcccaaagatgtgcttcaa 588
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Pred. No. 12;
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/db_xref="taxon:3055"
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The CDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"
169 c 163 g 93 t 1 others
                                                                                                                                                                                                                                                                   Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Razusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
LocatLon/Qualifiers
1. :529
/organism_"Chlamydomonas reinhardtii"
                                    Eukaryota: Viridiplantes: Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 529)
Asamizu.E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K., Nakamiza,Y. and Tabata.S.
Generation of expressed sequence tags from low-CO2 and high-CO2 bunk Res. 7 (5), 305-307 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3055"
/clone="LCL059f01_r"
/clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
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Chlamydomonas reinhardtii
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                    ORGANISM
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COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                              REFERENCE
                                                                                                                        AUTHORS
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SOURCE
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 Query Match
 4.0%; Score 34.8; DB 31; Length 529;

 Best Local Similarity 50.0%; Pred. No. 13;

 Matches 87; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

 Oy 415 ggagcggtaacccgtgaacccgtgagcggatgtgaagtagtagaaccttggaacc 474

 Db 405 GTACCAGATCGCGTTCCACTCGCGGGGGTTGAAGCCTATGTTGTAGC 346

 Oy 475 atggagcacttgGCGTTGCACTCGCGGGGTGAAGCTATTTGAA 286

 Oy 475 atggagcacttgGCGCTTCTGGTCGATGGGGGGGGAATGTTCTTGAA 286

 Oy 535 ctagattggagaggGGGCGTTGGTCGGTCGATGGGGGGGGAATGTTCTTGAA 286

 Oy 535 ctagattgggGTGGTGTGAACTGGGGGGGGATGGTGCCAAAGGGTGTTGTCCAA 232

 Db 285 CACGTTCCAGGGTACTTGAAGTGCTGGGCGGACCAAAGGGTGTTGTCCCA 232

Search completed: September 14, 2001, 06:59:27 Job time: 12074 sec Appli Appli Appli Appl

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Appli Appli Appl Appl

Scoring table:

Searched:

Database

Perfect score:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,878
                                     US-09-385-028-15
US-07-867-194-3
US-07-867-194-4
US-07-867-194-5
US-08-927-219-50
US-08-927-219-130
US-08-170-0958-3
US-08-170-0958-3
US-08-444-6868-5
US-08-444-6868-5
US-08-444-6868-5
US-08-444-6868-5
US-08-315-882A-15
US-08-318-1175A-3
US-08-318-1175A-3
US-08-318-1175A-3
US-08-318-1175A-3
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Pred. No. 8.3e-28;
0; Mismatches 409
                     -037-230D-23
                                                                                                                                                                                                                                                                                                                                                          US-08-463-160B-5
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STREET: One Market Plaza, Steuart Street
STREET: Ploor
CITY: San Francisco
STATE: California
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REGISTRATION NUMBER: .38,498
REFERENCE/DOCKET NUMBER: 15371A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/08390878 Patent No. 5700683 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543/9600
TELEFAX: 415/543/5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415/543/5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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49.9%;
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 15239 base pairs TYPE: nucleic acid
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Best Local Similarity 49.9
Matches 426; Conservative
                                                          213
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278
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MOLECULE TYPE:
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                                                                                                                                             ; Search time 93.36 Seconds
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/cgnl_7/ptodata/1/ina/5B_COMB.seq:*
/cgnl_7/ptodata/1/ina/6A_COMB.seq:*
/cgnl_7/ptodata/1/ina/6B_COMB.seq:*
/cgnl_7/ptodata/1/ina/pcTUS_COMB.seq:*
/cgnl_7/ptodata/1/ina/pcTUS_COMB.seq:*
                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-205-697A-18
PCT-US95-02576-18
US-08-685-625A-5
                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-751-767A-5
US-08-153-262-1
US-08-479-744A-28
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PCT-US95-02576-27
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US-08-142-368A-23
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US-08-793-900-1
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US-08-456-104-5
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                                                                                                                                             September 14, 2001, 07:51:13
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                                                                                                    · nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Match Length
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Score

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Result

4;

Gaps

30.

1405.0030001

FILING DATE: 15-DEC-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET UNMBER: 1405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600

LENGTH: 2058 base pairs

nucleic acid

STRANDEDNESS:

TOPOLOGY:

linear

CDS 751..1611

15-DEC-1994

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,

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TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2610
INFORMATION FOR SEG ID NO: 1.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-08-358-117-1
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                   5373 CAGGIGCIGGIGGICAGGGAAAAGCCAIGICGGGCGACGACGCAGGIAICCCGCIGIIG
                                                                                                                                              193 caagcagcgcggaaaatggtgttgctgcaagcagaaactaaagcgcaactatctgg--ac
                                                                                                                                                                                                                                           tttcctcccgtgttcaacgaggtagcttcttgggggtggagcaacgctcacgctgcgcttg
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                                                                         cgagtgttggtatcgcgcacccaaccggccaaagcaaccgaagcgggtgaagtccttgtg
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MICROORGANISMS AND PLASMIDS FOR 2,4-DI MONOOXYGENASE 2,4-DICHLOROPHENOXYACETIC ACID (2,4-D) MONOOXYGENASE FORMATION AND PROCESS FOR THE PRODUCTION OF THESE PLASMIDS AND STRAINS
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                                                                                                                                                                           73 ctttccatttccccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt 132
                                                                                                                      13 caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc 72
                                                                                                                                                                                                                      470 CTGCATATTTCCCAGCCCCCGGTCACGCGACAGATTCACGCGCTCGAACAGCATCTGGGC
Length 2058,
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PatentIn Release #1.0, Version #1.30
  Score 37; DB 1;
Pred. No. 0.073;
                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROMMER LAWRENCE & HAUG LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: STREBER, WOLFGANG R.
APPLICANT: TIMIS, KENNETH N.
APPLICANT: ZENK, MEINHART H.
TITLE OF INVENTION: MICROORGANISMS AN
TITLE OF INVENTION: 2,4-DIGHLOROPHENO
TITLE OF INVENTION: FORMATION AND PRO
TITLE OF INVENTION: RABINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/470,588
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                                                                                                                                                                                                                                                                                                        410 GIGITGITGITCGAGCGCAGC 390
                                                                                                                                                                                                                                                                 133 cgagtgttggtatcgcgcacc 153
  4.2%;
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                                             Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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  Query Match
                                             Matches
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APPLICANT: Kaphammer, Bryan J.
TITLE OF INVENTION: tfdA Gene Selectable Markers in Plants and the TITLE OF INVENTION: Use Thereof
TITLE OF INVENTION: Use Thereof
CORRESPONDENCE: 2
CORRESPONDENCE ADDRESS: ADDRESS: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.

COUNTRY:

Sequence 1, Application US/08358117 Patent No. 5608147 GENERAL INFORMATION:

US-08-358-117-1/c

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GENERAL INFORMATION:
APPLICANT: Sharpe, Arlene H.
APPLICANT: Boriello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Realer, Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
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                                                                                     28123 GAGGTCGTCGAGGAGCGAGGACCACGCCGGTGAAGCCGTCGCCGGTCGTCAGTGCGGTGAG 28064
                                                                                                                                466 cttggaaccatgcgccacttggccattgcaacccctcattgcgggatgcctacatggtt 525
                                              406 gatgttttaggagcggtaacccgtgaagctaatcccgtggcgggatgtgaagtagtagaa 465
    Gaps
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  0; Mismatches 145; Indels
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Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 27883 ACGCCAGTCGTCGCCGCCTGGTGGG 27857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text
CURRENT APPLICATION "DATA:
APPLICATION NUMBER: US/08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  646 gtcccgtcggcggaaggttttggtgag 672
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27, Application US/08205697A Patent No. 6218510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 108; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic
STRANDEDNESS:
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US-08-205-697A-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT SHIEST, Gary
APPLICANT SHIEST, Gary
APPLICANT SHIEST, Gary
APPLICANT SHIEST, Melanie C.
APPLICANT BETLACH, Mary C.
APPLICANT BETLACH, Mary C.
APPLICANT TANG, L1
TITLE OF INVENTION. RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
TITLE OF INVENTION. RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE SHEERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-08-28
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1998-05-08
EARLIER FILING DATE: 1998-05-28
EARLIER FILING DATE: 1998-05-28
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                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 2058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 3;
Pred. No. 0.073;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/09320878A Patent No. 6117659 GENERAL INFORMATION:
                                    ATTORNEY/AGENT INFORMATION:
NAME: LANRENCE, WILLIAM F.
REGISTRATION NUMBER: 28,029
REFERENCE/DOCKET NUMBER: 5144
TELEPHONE: 212-588-0800
TELEPHONE: 212-588-0500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Streptomyces venezuelae US-09-320-878-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 cgagtgttggtatcgcgcacc 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410 GTGTTGTTGTTCGAGCGCAGC 390
                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-470-588-1
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.2%;
Best Local Similarity 53.9%;
Matches 76; Conservative 0
                                                                                                                                                                       TELEFAX: 212-588-0500 INFORMATION FOR SEQ ID NO: 1:
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07-JUN-1995
4: 800
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                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
FILING DATE: 07
CLASSIFICATION:
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181 gaagteettgtgeaageagegeggaaaatggtgttgetgeaageagaaactaaagegeaa 240
                                                                                241 ctatctggacgccttgctgaaatcccgttaaccatcgccatcaacgcagattcgctatcc 300
                                                                                                                                                              301 acatggtttcctcccgtgttcaacgaggtagcttcttggggtggagcaacgctcacgctg 360
                                                                                                                     270 GAAAGGAGAGGGATGCCAGCCATCTTGTAACTGTTCAGCTTAATCTGAAAGAGGTTTTTA 211
                                                                                                                                                                                                     210 AGAAGGTGAGGTAGTGGGTAAAACAGCTTAAATTTGTTAAGGGAAGAATGCCTCATGATC 151
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                                       330 GATGGCAGAATGGAAACATGGCAAAAGAAGAGGTTACATTAAGCAAATTGCATATGGGGA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules TITLE OF INVENTION: and Uses Therefor NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                            3.8%; Score 33; DB 5; Length 379; ilarity 46.4%; Pred. No. 0.6; Conservative 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: BWI-120CPPC
TELECOMMUNICATION INFORMATION:
TELECHNIC (617)227-7400
TELECHNIC (617)227-5941
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02576
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                    PCT-0595-02576-27/c; Sequence 27, Application PC/TUS9502576; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 379 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
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Matches 108; Conserva
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STATE: Massac
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PCT-US95-02576-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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241 ctatctggacgccttgctgaaatcccgttaaccatcgccatcaacgcagattcgctatcc 300

330 GATGGCAGAATGGAAACATGGCAAAAGAAGAGGTTACATTAAGCAAATTGCATATGGGGA 271

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270 GAAAGGAGGAGGGATGCCAGCCATCTTGTAACTGTTCAGCTTAATCTGAAAGAGGTTTTTA 211
                                                                     301 acatggittcctcccgigitccaacgaggiagcitctiggggiggagcaacgcicacgcig 360
                                                                                                              210 AGAAGGTGAGGTAGTGGGTAAAACAGCTTAAATTTGTTAAGGGAAGAATGCCTCATGATC 151
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Slavsubramanian
APPLICANT: Baskar, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                361 cgcttggaagatgaagcgcacacattatccttgctgcggcgtggagatgtttt 413
                                                                                                                                                                                        LOCATION: 318 to 1181 bp IDENTIFICATION METHOD: similarity to other pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Open reading frame (translated region)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/147,772
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08147772 Patent No. 5858776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: CDNA in pCDM8 vector
CLONE: B7, Raji clone #13
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MANDERS, AND E. REGISTRATION NUMBER: 36,207
REFERENCE/POCKET NUMBER: RP
TELECOMMUNICATION INFORMATION: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
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APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE: lymphoid
CELL TYPE: B cell
CELL LINE: Raji
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boston
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                                                                                                                                                                                                                                                                                 RESULT 7
US-08-147-772-1/C
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1442 GATGGCAGAATGGAAACATGGCAAAAGAAGAGGTTACATTAAGCAAATTGCATATGGGGA 1383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1322 AGAAGGTGAGGTAGTGGGTAAAACAGCTTAAATTTGTTAAGGGAAGAATGCCTCATGATC 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 gaagtccttgtgcaagcagcgggaaaatggtgttgctgcaagcagaaactaaagcgcaa 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 ctatctggacgccttgctgaaatcccgttaaccatcgccatcaacgcagattcgctatcc 300
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APPLICANT: Nadler, Lee M.
APPLICANT: Gary Gary S.
TITLE OF INVENTION: No. 5942607el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSEE: STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 2; Length 149
Pred. No. 1.1;
0; Mismatches 125; Indels
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                                                                       REGISTRATION NUMBER: 36,207
REPERRINGE/COCKET VINBABER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
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FILING DATE: 26-JUL-1993
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
  19-AUG-1993
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APPLICATION NUMBER: 19-AUG
ATTORNEY/AGENT INFORMATION:
NAME: MANGERANDES: AND E.
REGISTRATION NUMBER: 36,20
                                                                                                                                                                                                                                                                                        STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 46.4
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        ; TISSUE TYPE: Iymphoid
; CELL TYPE: B cell
; CELL LINE: Raji
US-08-456-104-5
                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                   nucleic acid
EDNESS: double
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MEDIUM TYPE: Floppy
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
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APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                  AUTHORS: FREEMAN, GORDON J.
AUTHORS: PREEDMAN, ARNOLD S.
AUTHORS: PREEDMAN, ARNOLD S.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.8%; Score 33; DB 2; Length 1491; Best Local Similarity 46.4%; Pred. No. 1.1; Matches 108; Conservative 0; Mismatches 125; Indels
                      NAME/KEY: Alternate polyadenylation signal LOCATION: 1474 to 1479 bp IDENTIFICATION METHOD: similarity to other pattern PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           1: FROM 1 TO 1491
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                  DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08456104
Patent No. 5861310
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           2714-2722
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                                                                                                                                                                                                                                                                                                                 JOURNAL:
VOLUME: 1
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Pred. No. 1.1;
0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 318 to 1181 bp IDENTIFICATION METHOD: similarity to other pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1474 to 1479 bp
IDENTIFICATION METHOD: similarity to other pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B7, A New Member Of The Ig Superfamily With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Open reading frame (translated region)
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                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapien
TISSUE TYPE: 1ymphoid
CELL TYPE: B cell
CELL LINE: Raji
IMMEDIATE SOURCE:
LIBRARY: CDNA in pCDM8 vector
CLONE: B7, Raji clone #13
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FREEMAN, GORDON J.
FREEDWAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
WHITMAN, JAMES F.
                                                            REFERENCE/DOCKET NUMBER: RPITELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPERX: (617) 227-541
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                       NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.8%;
Best Local Similarity 46.4%;
Matches 108; Conservative (
ATTORNEY/AGENT INFORMATION: NAME: Mandragouras. Amv
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JOURNAL: The
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AUTHORS:
AUTHORS:
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TITLE: B
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1382 GAAAGGAGAGGGATGCCAGCCATCTTGTAACTGTTCAGCTTAATCTGAAAGAGGTTTTTA 1323
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                                                                               APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
UNBARE OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA PAPLICATION NUMBER: US/08/751,767A FILING DATE: 08-NOV-1996
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/08/751,767A
08-NOV-1996
                                                                                                                                                                                                                                                  ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-751-767A-5/c
;. Sequence 5, Application US/08751767A
; Patent No. 5994104
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Patent No. 6071716
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
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TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 46.4'
Matches 108; Conservative
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STRANDEDNESS: double
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                                                                             GENERAL INFORMATION:
APPLICANT: ANDERS
                                                                                                                                                                                                                                                                                                   ARLINGTON
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1322 AGAAGGIGAGGIAGAGGIAAAACAGCIIAAATITGITAAGGGAAGAATGCCICAIGAIC 1263
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Pred. No. 1.1;
0; Mismatches 125; Indels
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APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and TITLE OF INVENTION: Uses Therefor NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
); DATE: 15-OCT-1989
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1491
US-08-153-262-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONTENT AFFLICATION DAYS

FILING DATE: June 7, 1995
CLASSIFICATION 1435
FILING APPLICATION DATE:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 3-NOV-1993
APPLICATION NUMBER: 08/101,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: LAHIVE & COCKFIELD, LLP 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-479-744A-28/c
; Sequence 28, Application US/08479744A
; Sequence 10, Application US/08479744A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Freeman, Gordon J.
                                                                                                                                           46.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1491 base pairs TYPE: nucleic acid
                                                                                                                 Query Match 3.8%
Best Local Similarity 46.4%
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boston
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STREET: 60
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                                        APPLICANT: NADLER, LEE M.

TITLE OF INVENTION: DNA Encoding B7, A New Member

TITLE OF INVENTION: Of The IGG Superfamily With Unique Expression On

TITLE OF INVENTION: Activated And Neoplastic B Cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
The Journal of Immunology
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                                                                                                                                                                                                                                                                                                 ZIP: 02115
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
COMPUTER: IBM Personal System 2; Model 30
                                                                                                                                                                                  E: The Dana-Farber Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/751,306
FILING DATE: 28-AGC-1991
ATTORNEY AGENT INFORMATION:
NAME: HART, JULIA D.
RECISTRATION NUMBER: 33132
REFERENCE/DOCKET NUMBER: DFCI-116.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-8900
TELEPHONE: (203) 255-8900
TELEPHONE: (203) 255-8906
TELEPHONE: (203) 255-8966
TELEPHONE: (203) 255-8966
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS/DOS
SOFTWARE: WOTGPERFECT 5.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE TYPE: 1ymphoid
CELL TYPE: B cell
CELL LINE: Raji
IMMEDIATE SOURCE:
LIBRARY: CDNA in pCDM8 vector
CLONE: B7, Raji clone #13
CCHOROSOME/SEGMENT: 3
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FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
WHITMAN, JAMES F.
NADLER, LEE M.
  FREEMAN, GORDON J. FREEDMAN, ARNOLD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: no ANTI-SPMCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapien
                                                                                                                                                                                                                                                        Massachusetts
U.S.A.
                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2714-2722
                                                                                                                                                                                                                                    Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                       ADDRESSEE:
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AUTHORS:
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AUTHORS:
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VOLUME: 1
                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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PAGES:
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B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells . The Journal of Immunology
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RELEVANT RESIDUES IN SEQ ID NO: 28: FROM 1 TO 1491
                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Batentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994
CLASSIFICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,007
REGISTRATION NUMBER: 36,007
REGISTRATION NUMBER: 36,007
REGISTRATION NUMBER: 36,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: RPI-004CP2 TELECOMMUNICATION INFORMATION:
                                                  ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: cDNA in pCDM8 vector
CLONE: B7, Raji clone #13
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
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NADLER, LEE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: lymphoid
CELL TYPE: B cell
CELL LINE: Raji
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBLICATION INFORMATION:
                           CORRESPONDENCE ADDRESS:
                                                                                                                        Massachusetts
                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2714-2722
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LIBRARY: CDNA
                                                                                                    Boston
                                                                                                                                                                     02109
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AUTHORS:
AUTHORS:
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                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VOLUME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FREEDMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GAACE
WHITWAN, JAMES F.
NADLER, LEE M.
BY, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells
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46.4%; Pred. No. 1.1;
tive 0; Mismatches 125; Indels
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US-08-280-757B-28/C
Squence 28, Application US/08280757B
Stephen No. 613016
GREERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Gray, Gary S.
APPLICANT: Greefield, Edward
APPLICANT: Greefield, Edward
APPLICENT: Greefield, Edward
TITLE OF INVENTION: Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Open reading frame (translated region)
LOCATION: 318 to 1181 bp
IDENTIFICATION METHOD: similarity to other pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Alternate polyadenylation signal LOCATION: 1474 to 1479 bp IDENTIFICATION METHOD: similarity to other pattern PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAGES: 2714-2722
; DATE: 15-OCT-1989
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-479-744A-28
                                                                                                                                                                                                                                                                LIBRARY: cDNA in pCDM8 vector CLONE: B7, Raji clone #13 POSITION IN GENOME:
                                               CDNA to mRNA
                                                                                                         ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: lymphoid
CELL TYPE: B cell
CELL LINE: Raji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.89
Best Local Similarity 46.49
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                 CHROMOSOME/SEGMENT: 3
FEATURE:
STRANDEDNESS: double
                      TOPOLOGY: linear
MOLECULE TYPE: CDN
HYPOTHETICAL: no
ANTI-SENSE: no
                         linear
                                                                                                                                                                                                                                         IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL:
VOLUME: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS:
AUTHORS:
TITLE: B7
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APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaulo
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1382 GAAAGGAGAGGGATGCCAGCCATCTTGTAACTGTTCAGCTTAATCTGAAAGAGGTTTTTA 1323
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                                                                                                                                                                                                                                                                                                                                                                              AUTHORS: FALL.
AUTHORS: SEGIL, JEFFALL.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: WHITMAN, JAMES F.
AUTHORS: WHITMAN, JAMES F.
AUTHORS: WHITMAN OF THE TOTAL SET A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8%; Score 33; DB 3; Length 1491;
46.4%; Pred. No. 1.1;
tive 0; Mismatches 125; Indels
                                                                                                                                                                                                 NAME/KEY: Open reading frame (translated region) LOCATION: 318 to 1181 bp IDENTIFICATION METHOD: similarity to other pattern
                                                                                                                                                                                                                                                                                                        LOCATION: 1474 to 1479 bp
IDENTIFICATION METHOD: similarity to other pattern
                                                                                                                                                                                                                                                                                         NAME/KEY: Alternate polyadenylation signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: LAHIVE & COCKFIELD 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/08205697A Patent No. 6218510 GENERAL INFORMATION:
                                                                 IMMEDIATE SOURCE:
LIBRARY: CDNA in pCDM8 vector
CLONE: B7, Raji clone #13
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 3
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                          FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 46.4 Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
TISSUE TYPE: lymp
CELL TYPE: B cell
CELL LINE: Raji
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STATE: Ma
COUNTRY:
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                                                                                                                                                      181 gaagteettgtgeaageagegegegaaaatggtgttgetgeaageagaaactaaagegeaa 240
                                                                                                                                                                                                                                         241 ctatctggacgccttgctgaaatcccgttaaccatcgccatcaacgcagattcgctatcc 300
                                                                                                                                                                                                                                                                                                                                   acatggtttcctcccgtgttcaacgaggtagcttcttgggggtggagcaacgctcacgctg 360
                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Blincher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SUGNENES: 4
CORRESPONDENCE ADDRESS:
                                                                     DB 3; Length 1491;
                                                                                     Pred. No. 1.1;
0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RELEASE #1.0, VETSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,135
                                                                     Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY CACHT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/147,772
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09159135
Patent No. 6149905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS.
                                                                   3.8%;
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LENGTH: 1491 base pairs
                                                                 Query Match 3.8'
Best Local Similarity 46.4'
Matches 108; Conservative
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ORIGINAL SOURCE:
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: Massachusetts
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APPLICANT: Ostrano
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US-09-159-135-1/c
  US-08-280-757B-28
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ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: BWI-120
REFERENCE/COCKET NUMBER: BWI-120
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7401
TELEPHONE: (617)227-75941
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDSS: double
TOPOLCCUE TYPE: CDNA
FEATURE:
NAME/KEY: CDS

LOCATION: 318:.1181
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Query Match

3.8%; Score 33; DB 4; Length 1491;

Best Local Similarity 46.4%; Pred. No. 1.1;

Matches 108; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

Qy 181 gaagtccttgtgcaagcagcgcggaaaatggtgttgctgcaagcagaaactaaagcgcaa 240

Db 1442 GATGGCAGAAGGAAGAAGAAGAGGTTACATTAAGCAAATTGGGGA 1383

Qy 241 ctatctggacgccttgctgaaacccgttaaccatcgccatcacagcagattcgctacc 300

Db 1382 GAAAGGAGGGATGCCAGCATCTTGTAACTGTAATCTGAAAGGTTTTTA 1323

qq

301 acatggttcctcccgtgttcaacgaggtagcttcttggggtggagcaacgctcacgctg 360

Search completed: September 14, 2001, 07:51:47 Job time: 12421 sec

F11501/60

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September 14, 2001, 03:41:38 ; Search time 2960.24 Seconds (without alignments) 3715.094 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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711
                                                                                      OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                            Title:
Perfect score:
Sequence:
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Run on:

Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

2688314

1344157 seqs, 7733874588 residues

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

Searched:

Database

9b_ba1:*
9b_ba2:*
9b_ba3:*
9b_in1:*
9b_in2:*
9b_in3:*
9b_on:*
9b_pat1:*
9b_pat1:*
9b_pl:*
9b_pl:* GenEmbl:* ..

em_fun:* em_htgo_hum:* em_ba1:* em_ba2:*

em_htgo_rod:* em_htg_hum1:* .hum4: em_htg_hum2 em_htg_hum3

em_htg_inv2:*
em_htg_other:*
em_htg_rod:* em_htg_hum7: em_htg_hum8: hum6:

em_hum2: em_hum3: em_hum4

em_hum5:*
em_hum6:*
em_hum7:*
em_in:* *: mo_me em_or:*

gb_sts2:* gb_sts3:* gb_sy:* gb_un:* em_pat:* em_ph:* em_ro:* em_sts:* em_sy:* em_pl:* em_un:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb_pr9:*
gb_ro1:*
gb_ro2:*
gb_in4:*
gb_pr10:*

gb_pr1:

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SUMMARIES

x96471 C.glutamicu A93933 Sequence 2 AXO63771 Sequence AXO63767 Sequence AL357613 Streptcomy ABO11413 Streptcomy B4849 Mycobacteria	186263 Sequence 17
CGLYSEG A93933 AX063771 AX063771 SCSF8 AB011413	186263
B	10
Query Match Length DB 1 100.0 2374 2 C 61.2 822 9 P 67.1 993 9 P 57.1 12070 1 P	15239
Query Match 100.0 100.0 61.2 57.1 11.4 10.1	6.8
No. Score 1 711 2 711 3 435 4 406 5 81.2 6 71.8	63.2
11t	ထ
Result No. 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

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<pre>CDS</pre>		gene 1025. 1126 /gene="1y8F" CDS 1025. 1726 /gene="1y8F" /colon start=1	/transl_table=11 /product="Lysine exporter protein" /protein_id="CAA65324.2" /db_xref="G1:1339787" /db_xref="SWISS-PROT:P94633"	/translation="MRIFITGLILGAGILGISGIDGINERGIIAVLIVCLI SDVFLFIAGTLGVDLISNAAPIVLDIMRWGGIAYLLWRAVMAAKDAMTNKVEAPQIIE ETEPTVPDDTFGSAVATDTRNRVRVEVSVDKQRVWVKPMIANIVLTVINDNAYLDA FVFTGGVGAQYGDTGRWIFAAGAASLIWFPLVGFGAAALSRPLSSPKVWRWINVV AVVWTALAIKLMIMG" gene complement (1723 - 2352)		/united-color of the color of t	PSISTINGWEED THE WAY THE PROCESS THE STANDING TO THE STANDING THE STAN	Query Match 100.0%; Score 711; DB 2; Length 2374; Best Local Similarity 100.0%; Pred. No. 2.7e-207; Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 1 gigicatogggcacggiiggticigtiicticaaigaictgiggcgciiccacctigiii 60 	Oy 61 gtcatggcgtctttcgctgccatgacggcaaaccataacaggtaagcgatgccaccccag 120 111111111111111111111111111111111	Oy 121 cgcataatatcgagcacgatcggcgcggcattggacaaagatcaacgcccaaggtgccg 180 	Oy 181 gcgatgaacaaaagacgtcagaaattaaacacacgagaagaaccgcaatgagtccttcg 240 	Oy 241 cgcttaattccttgtttaatcaccagtacattctgcggtccgatggacagtaaaagactg 300 	Oy 301 gccccaaaagcagacctgtaatgaagatttccatgatcaccatcgtgacctatggaagt 360
1 AE005522 2 AP002563 3 MTCM309 9 AX030085 2 ECFDAPGK 1 AE000375 1 AE004852	7.4 1804 2 7.4 1815 2 7.4 10000 66 7.2 10367 1 6.9 11168 1 6.5 1657 1	6.2 37218 3 MTCX20G9 6.2 37218 3 MTCX20G9 6.1 6362 1 AF037440 6.0 14799 1 AF004916 6.0 13193 1 AF005455	6.0 268857 2 AP002560 5.9 4532 3 SYOSRRA 5.8 4033 2 ASU65741 5.7 10010 1 AE0044639 5.6 10239 1 AE004457	5.6 183704 67 AC023024 5.6 2878 2 AHAHYGENE 5.5 160938 77 AC090056 5.5 1033 1 AB053349 5.5 4217 2 AY017305 5.4 1070 3 PSECATRA	5.3 11015 1 AE004736 AE004736 Pseudomo 5.2 1644 1 AF061070 AF061070 S.2 10614 1 AE004351 AE004351 Vibrio e 5.2 18711 88 AC087244 AE004 S.2 18711 88 AC087244 AE004 S.2 18712 S.2 18712 S.2 18713 S.2	S.2 1790 3 PUPTEDRII ALIGNMENTS	CGLYSEG 2374 bp DNA BCT 18-MAR-2001	X96471.1 GI:1729753 lysE gene; lysG gene; Lysine export regulator protein; Lysine exporter protein; Lysine governor. Corvebacterium d'lutamicum	Corynebacterium glutamicum Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae;	<pre>Loryingarer 1 to 2374) Vrljic,M., Sahm,H. and Eggeling,L. A new type of transporter with a new type of cellular function: L-lysine export from Corynebacterium qlutamicum</pre>	Mol. Microbiol. 22 (5), 815-826 (1996) 97126810 2. (bases 1 to 2374)	Vrllc.M.M. Direct Submission Submitted (07-WAR-1996) M.M. Vrljic, Institut fuer Biotechnologie 1, Forschungszentrum Juelich, Postfach 1913, D-52425 Juelich, FRG Location/Oualifiers		complement(82954)
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ogcttaattccttgtttaatcaccagtacattctgcggtccgatggacagtaaaagactg [879 541 819 601 759	Oy 661 gctgaaatcccgttaaccatcgacatcaacgcagattcgctatccacatgg 711 bb 699 GCTGAATCCCGTTAACCATCGCCATCAACGCAGATTCCACATGG 649 RESULT 3 Ax063771/c LOCUS Ax063771 822 bp DNA PAT 24-JAN-2001 DEFINITION Sequence 53 from Patent W00100843. PAT 24-JAN-2001 VERSION Ax063771.1 G1:12541483 KEVWORDS.	Corynebac Bacteria; Actinomyc Corynebac Corynebac F Pompeias S Pompeias Corynebac proteins L Patent: W	Source 1	/translation="MEIFITGLLLGASLLLSIGPONVLVIKQGIKREGLIAVLLVCLI SDVFLEIAGTLGVDLLSNAAPTVLDIMRWGGTAYLLMFAVMAKDAWINKVERPQIIE ETEPTVPDDTPLGGEAVATDTRNRVRVEVSVKVKVKPMLMAIVLTWLNPNAYLDA FVFIGGVGAVGTOTRNFRAGAFAASLIWFPLVGFGAAALSRPLSSFKVWRNINVVV AVVMTALAIKLMLMG" BASE COUNT 167 a 192 c 246 g 217 t	Query Match 61.2%; Score 435; DB 9; Length 822; Best Local Similarity 100.0%; Pred. No. 1.6e-122; Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1059 361 999 421 939 879 879 819	Oy 601 gcagcggaaaatggtgttgctgcaagcagaactaaagcgcaactatctggacgctt 660	A93934/C LOCUS A93933 2374 bp DNA DEFINITION Sequence 2 from Patent W09723597. ACCESSION A93933 VERSION A93933.1 GI:6742037 KEYWORDS SOURCE COTYNEbacterium glutamicum. ORGANISM Bacteria; Firmicutes; Actinobacteriaceae; Corynebacterium. Corynebacterium. Actinomycetales; Corynebacterium. Corynebacterium. Corynebacterium. Actinomycetales; Corynebacterium. Actinomycetales; Corynebacterium. REFERENCE 1 (bases 1 to 2374)	*AUTHORS VILIGO, M. and Eggeling, L. *TITLE PROCESS FOR THE MICROBIAL PRODUCTION OF AMINO ACIDS BY BOOSTED ACTIVITY OF EXPORT CARRIERS ACTIVITY OF STATOR CARRIERS FEATURES **FEATURES** **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF AMINO ACIDS BY BOOSTED ACTIVITY OF STATOR CARRIERS **LOCATION OF ACTIVITY OF ACTIVITY OF STATOR CARRIERS **LOCATION OF ACTIVITY OF ACTIVI	Duery Match 100.0%; Score 711; DB 9; Length 2374; Best Local Similarity 100.0%; Pred. No. 2.7e-207; Matches 711; Conservative 0; Mismatches 0; Indels 0; Ga 1 gfgtcatcgggcacggttggttcfgttcttcaatgatctgtgggcgcttccaccttgttt Ill	Oy 61 gtcatggcgtctttcgctgccatgacggcaaaccataacaggtaagcgatgccaccccag 120	<pre>Qy 181 gcgatgaacaaaaagacgtcagaaattaaacacacgagaagaaccgcaatgagtccttcg 240</pre>

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Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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Submitted (05-JUN-2000) Streptomyces coelicolor sequencing proje
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                       1 CAAAAGCAGACCTGTAATGAAGATTTCCATGATCACCATCGTGACCTATGGAAGTACTTA 60
                                                            caaaagcagacctgtaatgaagatttccatgatcaccatcgtgacctatggaagtactta
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Thomson,N.R., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
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Mol. Microbiol. 21 (1), 77-96 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 1.4e-113;
                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCDF8 33285 bp DNA Streptomyces coelicolor cosmid 5F8.
              Pred.
100.08; Pr. 0;
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Unpublished
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                             Conservative
         Best Local Similarity
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ACASTACE = 01:12541480"
/translation="WHOTOLDTLSTIDEGSFEGASIALSISPSAVSQRVKALEHHVG
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RVLVSRTQPAKAT=AGEVLVQAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTW
BPDVRNEVASWGGATTLTRLEDEAHTLSLLRRODVLGAVTRENNVPVGCEVBLGTMR
HLAIATPSLRDAAMOKLDMAAMPVLRFGFRDVLQDRDLDGRVDGPVGRRRVSIVPS
AEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILLDBIPDTPWWQRWRLESRSLARL
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                                                                                         gtcatggcgtctttcgctgccatgacggcaaaccataacaggtaagcgatgccacccag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum.
Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria;
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BASF AKTIENGESELLSCHAFT (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX063767 993 bp DNA
Sequence 49 from Patent WO0100843.
AX063767
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/note="RXA01393"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AX063767.1 GI:12541479
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AX063767

RESULT

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source

FEATURES

CDS

BASE CO ORIGIN

AUTHORS TITLE

REFERENCE

JOURNAL

project,

1

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Complement(1287. .1328)
/gene="SC5F8.02c"
/note="SS01065 Serine/threonine dehydratases
pyridoxal-phosphate attachment site"
complement(1477. .2154)
/gene="SC5F8.03c"
/note="SC5F8.03c"
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/note="SC5F8.03c"
/note="SC5F8.03c"
/note="SC5F8.03c"
/note-"SC5F8.03c"
/note-"S
                                                                                                                                                                                                                        PARSVEIABEBAGALVRLTDGMDSAFALVTRLREEGLTLVHPFDDPVVVAGQGTVGLFF
BEDSBLTLTBCAPSVSRLTVDHVAELVALVRCVRWGVETERGABAMSRALAAGGPLT
VPLSSVVTTLGAPSVSRLTVDHVAELVTEVLVVPDRRAVRGSLALAEHAKVWTEPAAG
CLLPAARRVVERVGDGARIGLVVCGGNATVGDMAVWADRFGLR
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FTVNGRNVLCFDASLSYRIATVKGSGIAGGGLFNSVFTGQGRLGLVCEGNPLVIPVSQ
OYPVHVDTDAVVGWSAGLATSLHRSQSIGSMLRGGSGBAVQLVLQGEGFVVVRPSEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MSDLVPGGNVPLPGGPVSVRVPGGFDVSALVTDEGGKVGGDADF
YFY NQPEAGARLRDDTLTVDPARLERGARVAVAGEBEDGFPLGALESPTVLVTDA
RGRYVARFTPARPGETVLLLYPEYRRGGRWYRALGOGYADGLAGLARDFGSYBYTDA
RGRYVARFTFARPGETVLLLYPEYRRGGRWYRALGOGYADGLAGLARDFGYBYTDD
APPEPATAPEDITPGADSDGFLNLVNSARAAGSPAVRPDPRLRSAARAHAAAAAG
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FTHAGWACVTGGPSGDTYWTALWAVPLTPDGLARTTAEVVGLTNRERAGAGLPALAVD
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QRTGSFKARGATAKLLSLTEAERAAGVVAVSGGNHGIAVAVWAAALDVKATVVWPRTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aa. Similar to several other putative regulators from Streptomyces coelicolor including:
TR:Q9XAN4 (EMBL:AL079355) SC4C6.06 (893 aa), fasta scores opt: 305 z-score: 318.7 E(1): 7.7e-11 26.4% identity in 910 aa overlap and TR:Q92573(EMBL:AL035569) SC8D9.18 (1091 aa), fasta scores opt: 857 z-score: 926.1 E(): 0 36.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MKGDLFSSEHMVQPATAPGMTVENSKCIRYAVNGEMLARQGAMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pyridoxal-phosphate dependent enzyme, score 210.10, E-value 3.3e-59"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               radiodurans TR:09kWP1(EWBL:AE001920) conserved hypothetical protein (254 aa), fasta scores opt: 46 z-score: 555.6 E(): 1.8e-23 36.6% identity in 205 coverlap and Streptomyces coelicolor (ZR:CAB70638(EWBL:AL137242) SCBF4.12C (239 aa), fast scores opt: 397 z-score: 474.2 E(): 6.1e-19 36.1% identity in 183 aa overlap."
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/protein_id="CAB93732.1"
/db_xref="G1:8347027"
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/db_xref="G1:8347026"
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complement'...
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/note="scene"
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/gene="SC5F8.04c"
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/gene="SC5F8.05c"
complement(3562. .6528)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(546. .1412)
/gene="SC5F8.02c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Junivey-Poin/Irameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, qtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5.13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. If may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid 5FB lies on genomic restriction fragment Asel-A bordered by cosmids 5HI and 4G10.
                                                                                                                                                                                                                  are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complement(422. .1451)
/gene="SCSFB.02c"
/gene="SCSFB.02c"
/note="SCSFB.02c"
/note="
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CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                         The more significant matches with motifs in the PROSITE database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dehydratases pyridoxal-phosphate attachment site and a Pfam match to entry PF00291 S_T_dehydratase, Pyridoxal-phosphate dependent enzyme."
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/db_xref="GI:8347024"
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/db_xref="taxon:100226"
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/gene="SC5F8.02c"
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/note="scre--
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/gene="SC5F8.01c"
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/gene="SC5F8.01c"
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1. .33285
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.nih.go.jp/
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/translation="Matqalgtalricyfdrictgelraealagslgthpratirler
Alaciollsbepergrettaagnvijandapotmvamarmetrowilergwblidesvrt
gettpotyfctdfffglirehpelsaarneamsggtritaetvphyxdfgrforlvdig
ggdottlasiilrahgergvledtaeglaoaprrlargiscidgrytefgrforlad
gdlyllinsiiihdddavrghirhirdvipdhgsllinsvedbrrabresdd
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ITTYSPLRRWGAGPGKKVAVVGLGGLGHMAVKIAHALGAEVTVLSQSLRKKDDGLKLG
ADHYYATGDPRTFEELAGTFDVILSTVSAPLDFGAYLALLRTEGTLVNVGAPEEPVSL
NLFSLILGNRSIAGSAIGGIEETQEMLDFCAVHGLGAEIEVIGAGQVNEAYERVLASD
                                                   TODRARMDAEYDEMRRRASVAASLVYYEDDRIRSAGPAEHRSLVLSLYIGAGALTALA
ALTGHYLGSRGCGPAMFALEDGERLLADAHEERTPYPYANKGSYEVAAGAPGGLEGOL
PRIRRAADRWADVYBYLLTRGRIEGARTSYGGRSRIRLDQLVEEVCAELPEGGFGLEST
LEESVVEADRAADKWAVRNLLLDNAVRHGPGSRGAAGRGRTAGDRVRTGVRVADRGPAV
                                                                                                                                                                                                                                                                                                                                                                   /translation="mrvllveddddlrdvigagramdcasdwpeadvllhlsa
YDCVVLDRWVPSGDTLAPLEGRRRAGWSVPVLCLTALDSLDBRLRGLESGADDYLARP
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LLVHRDTVVTRTGLLEHCWDBRADPVSNVVDAVVAGLRRKLGSPGLVHYVRGGFELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protesin_id="Baa32133.1"
/db_xref="G1:3401950"
/db_xref="G1:3401950"
/translat_ion="MSELPLDQVRTLLAVVDEGTFDSAATALRLTPSAVSQRVKALEQ
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LATWSWQPCGACRRSWDSATTAPGGPGPYGRPAAGGAGDGRGDLVAGGGDGLFGPAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RMRYLPVASPGFADRWLGRRDGTALRELIGEAPVVCFDRRDDLQDAFVRRLGPGARPS
ARRHLVPTSEGFANAVASGMGMVPEVQAEPLLSDGRLVRLAPEPTVDVPLYWQQMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGGEPTEIGLEVFCSDLKWRAGLPAQGRVGWAVHRGDRLAATGVAATRFSTPKAYRRM
RGDVPVEGISLPETAPVPASPAGRARVEDVVLSGTGREGVWELRVDTRHPTLFQRPND
HVPGMLLLEAARQAACLVAGPAGIVPVEARTRFHRYSEFGSPCWIGAVVQPGADEDTV
                                /translation="VAAPVPAAPHPGPEAAAPAAARLTAAYTLITVVGLACLSWLVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MDAEAEVVHPVGIEMVHRTRPEDAFPRNWVRLGRDRFAVEAVLP
HDHPFFAPVGDDLHDPLLVAEAMRQAAMLAFHAGYGIPLGYHFLLTELDYVCHPEHLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MTTVAAYAAPRAKAPLERTTIERRPVGEFDILIDIKFAGICHSDIHQARDGWGEGIFPWVPGHEIAGIVAETGPGVTRFKVGDRVGVGCMVDSCGTCDACLM
                                                                                                                                                                                                               /function="two-component regulator protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="alcohol dehydrogenase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4333. .>5250)
/function="methyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="regulator protein"
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/transl_table=11
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/protein_id="BaA32134.1"
/db_xref="GI:3401951"
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10558. .11598
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/protein_id="BAA32135.1"
/db_xref="G1:3401952"
                                                                                                                                                                                                                                                                                         /product="Orf3"
/protein_id="BAA32131.1"
/db_xref="G1:3401948"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Orf4"
/protein_id="BAA32132.1"
                                                                                                                                                                                 complement(3523. .>4197)
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/transl_table=11
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/transl_table=11
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/transl_table=11
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/transl_table=11
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ORIGIN
identity in 1077 aa overlap. Contains a Prosite hit to PSO0017 ATP/GTP-binding site motif A (P-loop) Pfam match to entry PF00196 GerE, Bacterial regulatory proteins, luxR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-FEB-1998) to the DDBJ/EMBL/GenBank databases. Takashi Umeyama, University of Tokyo, Department of Agriculture and Life Sciences; Yayoi 1-1-1, Bunkyo-ku, Tokyo 113, Japan (E-mail:aa67103@hongo.ecc.u-tokyo.ac.jp, Tel:+81-3-3812-2111)
                                                                                                                                                                                                                                                                                                               DLLRPLLGRGVLQRPAGGAPGHRLALPASYRADDLHRRHPLRPLLAELVRLPGVERLE
LRPLPDSDVARLVRLLRERRLPDSTVRRIVERAEGNAFYAEELVAATDAPAGGVPSGL
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                                                                                                                                                                                                                                                                                         GHPVADRLLGGGPDDGTDAAPSRLRLFEGVAALLTELADVAPLLLVLEDLHWADQSSR
                                                                                                                                                                                                                                                                                                                                                                     ADVLLIRFEQLSETAQQVLRTAAVAGRRVGHDLLRDAVGLPEELESALREAVERQLL
                                                                                                                                                                                                                                        /translation="MGGVPQTSLTSPLVGREDELARLTGVLERARAGEARAVLVAGDA
                                                                                                                                                                                                                                                                GVGKTRTLHEAAGRAAAAGTTVLTGHCVDLGDVGLPYLPFTEILGVLAADERFAAVLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Orf8; AfsA; Orf5; Orf4; Orf3; Orf2.
Streptomyces griseus DNA.
Streptomyces griseus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces 1 (bases 1 to 12070)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18032 CTGCACGTGACGCCGTCCGCGGTCAGCGGGGGGGAGCACCGGAGCGCCGCCTCCGGC 17973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17972 CGGTGCTGCTGCTGCGCACCAAGCCGGTGCGGGCGACCGATTCCGGCGCGCGTGCTGGTG 17913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctttccatttccccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgagtgttggtatcgcgcacccaaccggccaaagcaaccgaagcgggtgaagtccttgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 33285;
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 81.2; DB 3; Length 3
Pred. No. 2.1e-13;
0; Mismatches 93; Indels
                                                                                                                                                           /product-"putative LuxR-family regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function="sensor histidine kinase"
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Open reading frame encoded around afsA gene
Unpublished (1998)

    12070
/organism="Streptomyces griseus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                    /protein_id="CAB93733.1"
/db_xref="GI:8347028"
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/protein_id="BAA32130.1"
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complement(2660. .3511)
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AB011413
AB011413.1 GI:3401946
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59.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137; Conservative
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Best Local Similarity
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Mycobacterium bovis deletion region 2, immunogenic protein (mpt64)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 14844)
Mahairas,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K.
Molecular analysis of genetic differences between Mycobacterium
J. Bacteriol. 178 (5), 1274-1282 (1996)
                                                                                                                                                             6642 CGCCGACGCCAGCGAACGACGAGCCCCGACGCGCGACCCCCAGCGCGATGAGCAC 6583
                                                                                                                                                                                                                                                                                                                                                                                                                                                          6283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6163
                                                                                                           6702 CGCGGCGAGCAGCCGTAACCGATCAGGAACACGGCGCCGAGCAGCCCCCACCACCGTGAG 6643
                                                                                                                                                                                                                          6582 CGCGTCGGACAGGCCCAGATCCCGACCACGCGAGAACGCCGTCGCGGCGGACGCCCTC 6523
                                                                                                                                                                                                                                                                                                                                         5462 ACCGGCGGCTGCTGTCGCCGTTCGTCATGCGGCGACGCTACGGAGCAGGAACCCC 6403
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1 (bases 10567 to 11392)

0ettinger, T. and Andersen, A.B.

Cloning and B-cell-epitope mapping of MPT64 from Mycobacterium tuberculosis H37Rv
                                                                                                                                        cacgatcggcgcgcattggacaaaagatcaacgcccaaggtgccggcgatgaacaaaaa 194
                                                                                cyctyccatyacyycaaaccataacayytaaycyatyccaccccaycycataatcyay 134
                                                                                                                                                                                               gacgicagaaattaaacaacgagaagaacgcaatgagiccitcgcgcttaaticcitig
                                                                                                                                                                                                                                                    6402 GGTGTCCAGCTAAAGATTCTTACGTATCATTAGCGCTCATGATGTCCGAGCTTCCTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                               416 ttcaactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttag
                                                                                                                                                                                                                                                                                                                                                                                                                                            315 acctgtaatgaagatttccatgatcaccatcgtgacctatggaagtacttaagtaaaatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccetttccatttcccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtcgagtgttggtatcgcgcacccaaccggccaaagcaaccgaagcgggtgaagtccttg
                                                     19;
                      Length 12070:
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                     Indels
                                                    0; Mismatches 267;
                         Score 71.8; DB 1;
Pred. No. 1.3e-10;
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94222581
                                                                                                                                                                                                                                                                                                                                                                      375 attggttcttaacatggtttaatatagcttca-----
                         10.18;
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U34849
U34849.1 GI:1049224
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                                   Similarity 47.7
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                                                  261;
                         Query Match
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//organism="Mycobacterium bovis"
/db_xref="taxon:1765"
2864..2888
/abc.2888
/note="none of two imperfect direct repeats located at or near the deletion breakpoints"
nce replace(2888..13674,"")
related, but avirulent strain Mycobacterium bovis BCG"
10705..11391
/done="mpt64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGOACQIQ
WARDAYUNINISLPSYYPDOKSLENT TAQTROKFLSAATSSTPREAPELANTTSATYQS
AIPPRGTQAVVLKVYQNAGGTHPTTTYTAQFDWDOARKPITYDTLWQADTDPLPVVFP
IVQGELSKQTGQQVSIAPNAGLDPVNYQNFAVTNDGVIFFFNPGELLPBAAGPTQVLV
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       and Stover, C.K.
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/note="one of two imperfect direct repeats located at
near the deletion breakpoints"
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Mahairas,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover Direct Submission
Submitted (24-AUG-1995) Mark J. Hickey, Molecular Micro.,
PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caagcagcgcggaaaatggtgttgctgcaagcagaaactaaagcgcaactatctgg--ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4979 CAGGTGCTGGTGGTCAGGGAAAAGCCATGTCGGGCGACGACGACGCAGGTATCCCGCTGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="immunogenic protein"
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US 5700683.
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Stover, C. Kendall and Mahairas, G.G.
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/db_xref="GI:1049225"
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N Sequence 17 from patent US
186263.1 GI:3306777
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                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="mpt64"
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Best Local Similarity 55.3%;
Matches 166; Conservative
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/db_xref="taxon:155864"
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Virulence-attenuating genetic deletions deleted from mycobacterium
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EDL933 genome, contig 3 of 3, section 141
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Perna, N.T., Plunkett,G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew,G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfal,G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7
Nature 409 (6819), 529-533 (2001)
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Escherichia coli 0157:H7 EDL933
Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                            5253 CAGCTGGCCGCATTGGCTGCTCGAACTGGGCAGCTTCGATGCGGCCGCGGGAGCGC
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/strain="EDL933"
/serotype="0157:H7"
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                8.9%; Score 63.2; DB 10;
55.3%; Pred. No. 6.1e-08;
tive 0; Mismatches 128;
                                       Patent: US 5700683-A 17 23-DEC-1997;
                                                              Location/Qualifiers
1. .15239
                                                                                                 /organism="unknown"
4791 c 4729 g
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Escherichia coli 0157:H7
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AE005522.1 GI:12517448
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Best Local Similarity 55.3
Matches 166; Conservative
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AUTHORS
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/function="phenotype; Not classified"
/note="Residues 1 to 331 of 331 are 99.69 pct identical to
residues 1 to 331 of 331 from Escherichia coli K-12 Strain
MG1655: B2918"
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ETEYARMYDCFISLQIAGGDDLQOIRKGLMEYADLLVINKDODDNHTWYAIARHMYE
SALHILRRKYDEWQPRYLCSALEKRGIDETWHAIIDFKTALTASGRLQQVRQQSVE
SALHILRRKYDEWGLAFYRQILLAVKNNTLSPRTGLRQLSEFIQTOYFD"
                                                                                                                                                                                                                                                               /note="Residues 1 to 714 of 714 are 99.15 pct identical to residues 1 to 714 of 714 from Escherichia coli K-12 Strain MG1655: B2917"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSNEQEWQQLANKELSRREKTVDSLVQQTAEGIAIKPLYTEADL
DNLEVTGTLPGLPPYVRGPRATMYTAQPWTIRQYAGFSTAKESNAFYRRNLAAGGKGL
SVAFDLATHRGYDSDNPRVAGDVGKTGVAIDTVEDMKVLFDQIPLDKMSVSWTMNGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPVLAFYIIAAEEQGVTPDKLTGTIQNDILKEYLCRNTYIYPPKPSMRIIADIIAWCS
GNMPRFNTISISGYHMGEAGANCVQQVAFTLADGIEYIKAAISAGLKIDDFAPRLSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGIGMDLFMNVAMLRAARYLMSEAVSGFGAQDPKSLALRTHCQTSGWSLTEQDPYNNV ITTIERALAATIGGTQSLHTHREPBAELGLFPTOSRARINGTIIQDEESELCRYUDPL AGSYY IESITDQIYGQARAITQOJDBAGGMARAIEAGLFBRAIEASAREQSILDQGR RVIVGVNKYKLDHEDETDVLEIDNWWYRNEQIASLERIRATRDDAAVTAALNALHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QHNENLLAAAVNAARVRATLGEISDALEAAFDRYLVPSQCVTGVIAQSYHQSEKSASE
FDAIVAQTEQFLADNGRRPRILIAKMGLDGHDRGAKVIASAYSDLGFDVDLSPMFSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEIDDLMQALSDLNRPEIRCIILRAPSGSKVFSAGHDIHELPSGGRDPLSYDDPLRQI
TRMIQKFPRPIISMVEGSVWGGAFEMIMSSDLIIAASTSTFSMTPVNLGVPYNLVGIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MINEATLAESIRRLRQGEHATLAQAMTLVESRHPRHQALSTQLL
DAIMPYCGNTLRLGVTGTPGAGKSTFLEAFGMLLIREGLKVAVIAVDPSSPVTGGSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
/product-"putative enzyme"
/protein_id="AaGs045.1"
/db.ref="G1571451"
/translation="MNLSRRNILIKGIFMSYQYVNVVTINKVAVIEFNYGRKLNALSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLTRÖAGFHIVKELIFTASPITAQRALAVGILNHVVEVEELEDFTLQMAHHISEKAPL
AIAVIKEELRVLGEAHTMNSDEFERIQGMRRAVYDSEDYQEGMNAFLEKRKPNFVGH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEIARLÄVENDVHVVGASSLAAGHKTLIPELVEALKKWGREDICVVAGGVIPPQDYAF
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/note="Residues 1 to 275 of 275 are 100.00 pct identical.
to residues 1 to 275 of 275 from Escherichia coli K-12
Strain MG1655: B2919"
                                                                                                                                                                                                /function="enzyme; Degradation of small molecules: Fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative nucleotide-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="methylmalonyl-CoA mutase (MCM)"
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2270. 3265
/gene="ygfD"
/note="enterohemorrhagic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAG58043.1"
/db_xref="GI:12517449"
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/db_xref="GI:12517450"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                              /gene="sbm"
/note="z4254"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2270. .3265
/gene="ygfD"
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/gene="ygfG"
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/gene="ygfG"
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/gene="ygfH"
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                                                                                                                                 133. .2277
/gene="sbm"
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Sasakawa,C. and Shinagawa,H. Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterchemorrhagic Escherichia coli O157:H7 Genes Genet. Syst. 74 (5), 227-239 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli 0157:H7 (strain:0157:H7, sub_strain:RIMD 0509952)
                                                                                                                                                /function="putative transport; Not classified"
/note="Residues 1 to 286 of 286 are 100.00 pct identical
to residues 1 to 286 of 286 from Escherichia coli K-12
Strain MG165: B2924"
/codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7922 CCAAAAATCCCCGCGCAAATCAGGACCAAATCGCTGATAGCGCAAAGTAAGGCAATCATA 7981
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be,H., Iida,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 atgccaccccagcgcataatatcgagcacgatcggcgcggcgttggacaaaagatcaacg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 tecacettgtttgtcatggcgtetttcgetgccatgacggcaaaccataacaggtaagcg 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-2001
FGLAILAAWLAPRLRTAKSQRIINLVVGCVMWFIALQLARDGIAHAQALFS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 atgagtocttogogottaattocttgtttaatcaccagtacattotgoggtcogatggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 cccaaggtgccggcgatgaacaaaaagacgtcagaaattaaacacacgagaagaaccgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7982 ATGTGGTACTGACGACGAATGCCCTGATTCATCACAAAAGCATTTTGTGGGCCGAGCGGC
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Ohnishi, M., Murata, T., Nakayama, K., Kuhara, S., Hattori, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.7%; Score 62; DB 1; Length 10701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                      /product="putative transport protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.3e-07;
0; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 agtaaaagactggccccaaaagcagacctgtaatgaa 326
                       complement(8230. 9090)
                                                                                                   .9090)
                                                                                                 complement(8230.
/gene="yggB"
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Escherichia coli 0157:H7
AP002563 BA000007
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                                                    /gene="yggB
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Matches 143;
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MEDLINE
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KEYWORDS
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                     /function="putative enzyme; Not classified" hoto="Residues 1 to 492 of 492 are 99.39 pct identical to residues 1 to 492 of 492 from Escherichia coli K-12 Strain MG1655: B2920"
                                                                                                                                                                                                                                                                                                                     LNHYHDPRVAELADIYIPGAPPRRINSYSIFHAMDRYGTRYQIDERKIYAYVETULAGANNALDKONPMCQQIADNVYFFLLQEMAHGRIPPEFLPLQSGVGNINNAVMARLGENP
BIPPPMWYSEVLQESVYHLLETGKISGASASSLISADSLEKKIYDNMDYFASRIYURP
GEINNPEIIRLGVIALWYGLFEDIYGHANSTHVAGVDLMNGIGGSGDFERNAYLSI
FMAPBIAKEKKISTYPWCSHYDHNBHSVKYITTEQGIADLAGLSPLQRARTIIDNCA
HPMYRDYLHRYLENAPGGHIHHDLSHVFDLHRNLIATGSMLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="putative regulator; Not classified"
fnote="Residues 1 to 192 of 192 are 99.47 pct identical to
residues 6 to 197 of 303 from Escherichia coli K-12 Strain
MC1655, p3921"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MDIFISKKMRNFILLAQTNNIARAAEKIHMTASPFGKSIAALEE
OGYTLETRKNNISLNKROQGELYQKLEPVYQRLSALDNEIHNGGRRGREIVIGIDNT
YPTIFDQLISLGORYEGYTAQPVEFSENGYIDNLFDRQLDFIISPQHYSARVQELEN
LTISELPPLRINFLVSRRYEBRQEQELLQELP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="yggA"
/function="orf; Unknown function"
/note="Residues 1 to 211 of 211 are 98.10 pct identical to residues 1 to 211 of 211 from Escherichia coli K-12 Strain MG1655: B2923"
                                                                                                                                                                                                                                                                         ANEQHEAKKPYQIRLLTGASISAAADDVLSDADAVSWRAPYQTSSGLRKKINQGAVSF
VDLHLSEVAQMVNYGFFGDIDVAVIEASALAPDGRVWLTSGIGNAPTWLLRAKKVIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATLAIEVNVAAKDAATAKKQADERVAQYISFLELNQIAKKDISSANLRTQPDYDYQDG
KSILKGYRAVRTVEVTLRQLDKLNSLLLDGALKAGLNEIRSVSLGVAQPDAYKDKARKA
AIDNAIHQAQELANGFHRKLGPVXSVRYHVSNYQPSPMVRMKADAAPVSAQETYEQA
                                                                                                                                                                                                                                                    /translation="METQWTRMTADEAAEIIQHNDMVAFSGFTPAGSPKALPTAIARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MKFKVIALAALMGISGMAAQANELPDGPHIVTSGTASVDAVPDI
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ISDLVLICAGIFGGSALLMQSPWLLALVTWGGVVFLLWYGFGAFKTAMSSNIELASAE
VLKQGRWKIIATMLAVTWLNPHVYLDTFVVLGSLGGQLDVXPKRWFALGTISASFLWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="phenotype, Not classified"
/note="Residues 1 to 246 of 246 are 100.00 pct identical
to residues 1 to 246 of 246 from Escherichia coli K-12
Strain MG1655: B2922"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11 /product="partial putative transcriptional regulator
                                                                                                                                     /transl_table=11
/product="putative coenzyme A transferase"
/protein_id="AAG58046.1"
/db_xrefe="G1:12517452"
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/protein_id="AAG58049.1"
/db_xref="G1:12517455"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIQFDDQVDVVFQLEPVDQQPAKTPAAQ" complement(7456. .8091)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative actin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAG58047.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(5878. .6456)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(6623. .7363)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(5878. .6456)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="24259"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="24258"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="yggE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="yggA
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gene

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IIAAEPPNPLVNELIIMPDIEKRLEAFVRIAHGIIFPGGVGTAEELLYLIGILMNPA
NYDQYLELIIGGPKESADYFRYLDEFVVHTLGENARRHYRII IDDAAEVARQMKKSMP
LVKENRRDTGDAYSFWRAPPDLQMPFEPSHENMANLKLYPDQPVEVLAADLRRAF
SGIVAGNVKEVGIRAIEEFGPYKINGDKEIMRRMDDLLQGFVAQHRWKLPGSAYIPCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence-not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to SYD_ECOLI gi|1789157 percent identity 98 in 181 aa (Conserved in E.coli K-12)" /codon_start=1 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /traislation="MSSYANHOALAGLTLGKSTDYRDTYDASLLQGVPRSLNRDPLGL
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LVSFRHHNEFHEQCVERIFNDLLRFCQPEKLSVYARYTRRGGLDINPWRSNSDFVPST
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GLSTDNSKELLSRFENFDINVLRRERGVKLELINPPEBAFVORSITEALAQANLFAVLR
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ENEYINARRYCHQLGLERELNICTGGGFFAMEAPAWGAAVGHAQORYKDSRFIGWTEPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="similar to YQCD_ECOLI gi|1789158 percent identity in 282 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 //note="similar to YGDH_ECOLI gi|1789159 percent identity
// in 454 aa (Conserved in E.coli K-12)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
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/note="inhibitor of CsrA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="csrB"
complement(2444. .2989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ECs3653"
complement(2444. .2989)
/gene="ECs3653"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="CsrB RNA"
                                                                                                          /codon_start=1
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/gene="ECs3655"
4017. .5381
/gene="ECs3655"
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3057. 3005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3057. .3905
/gene="ECs3654"
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                                                                                                                                                                                                                                                                                                                        LFADDAS"
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                                                                                                                                                                                                   Complete nucleotide sequence of the prophage VTI-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli O157:H7 strain derived from the Sakai outbreak Gene 258 (1-2), 127-139 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:ken@gen-info.osaka-u.ac.jp, Tel:81-6-6879-8365, Pax:81-6-6879-2047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MAEIGIFVGTMYGNSLLVAEEAEAILTAGGHKATVFEDPELSDW
LPYQDKYVLVVTSTTGQGDLPDSIVPLFQGIKDSLGFQPNLRYGVIALGDSSYVNFCN
GGKQFDALLQEQSAQRVGEMLLIDASENPEPETESNFWVEQWGTLLS"
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VLBELDKITADRFAREDKGROPAVHTHYGLATVEMPVATGRYPTRYGLVELEERTGR
KHOLRRHLAHLRHPITGDSKHGDLRQNRSGABHFGLQRLMLHASQLSLTHPFTGEPLT
IHAGLDDTWMQALSQFGWRGLLPENERVEFSAPSGODGERSS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to B2790_ECOLI gi|1789154 percent identity
100 in 149 aa (Conserved in E.coli K-12)"
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/note="similar to YQCB_ECOLI gi|1789155 percent identity
99 in 260 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohnishi, M., Kurokawa, K., Makino, K., Yasunaga, T., Shinagawa, H. and
                                                                                                 Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S.,
Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                                                                                            Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K.,
Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Ilda,T. Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
20557356
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/gene="ECS3650"
complement(244, .693)
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/gene="ECs3652"
complement(1493. .1822)
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                                                                                                                                                                                             Shinagawa, H.
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Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique
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MSDAYNINISLPSYYPQSKSLENTIAQTROKFLSAATSSTPRBAPYEENITSATYQS
MIPPRGTQAVVLKVYQONAGGTHTTTYKARDDWQAXRKPITVDTLUMQADTDPLEVVYP
IVQGELSKQTGQQVSIAPNAGLDPVNYQNFAVTNDGVIFFRNDGELLPBAAGPTQVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct
                                                                                                                                                                                                                                                                                                                                                                                                               Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France B-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Rv1981c, (MTCX39.38), ribonucleotide reductase small subunit, len: 322, highly similar to RIR4_SALTY P17424, ribonucleoside-diphosphate reductase (319 aa) FASTA scores, opt: 1402, z-score: 1716.0, E(): 0, (66.0% identity in 315 aa overlap); Also similar to Rv3048c, (MTV012.63c); containsPS00368 Ribonucleotide
   Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MPBG_MYCBO P19996 immunogenic protein mpb64/mpt64 (228 aa).Similar to Rv3036c, (MTV012.51c)"
   Squares,S., Sqares,R., Sulston,J.E., Taylor,K., Whitehead,S. ar
Barrell,B.G.
Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Jun 27, 1998 this sequence version replaced gi:1403436
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                                                                                                                                                                          Erratum:[[published erratum appears in Nature 1998 Nov
12;396(6707):190]]
2 (bases 1 to 38500)
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                                                                                      complete genome sequence
Nature 393 (6685), 537-544 (1998)
98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(968. .1936)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:1773"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(91. 777)
/gene="mpt64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(91. .777)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="Y39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="nrdF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="nrdF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .38419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRSAIDSMLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .38500
                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Initiation codon.
                                                                                                                                                                                                                                                                 Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                     JOURNAL
                                                                                                                                                    MEDLINE
                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
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                                                                                                                                                                                REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DD 161484 ATGTGGTACTGACGACGAATGCCCTGATTCATCACAAAGCATTTTGTGGGCCCGAGCGGC 161543 · · ·
                                                                                                                                                                                                                                                                                                                                                                                AGVGGMIPLIIMAILAFPMTFFAHRGITRFVLSGKNPGEDITEVVEEHFGIGAGKLIT
LLYFFAIYPILLVYSVAITNTVESFWSHQLGMTPPPRAILSLILIVGMMTIVRFGEQM
IVRAMSILVFPFVGVLMLLALYLIPQWNGAALETLSLDTASATGNGLMWTLWLAIPVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLAAAKEQNISILSYLANHFNAPVIAWAPIIAIIAITKSFLCHYLGAREGFNGWVIK
SLRCKGKSIEINKLNRITALFMLVTTWIVATLNPSILCMIETLGGPIIAMILFLMPMY
AIQKVPAMRKYSCHISNVFVVVWGLIAISAIFYSLFS"
                                                                                                                                                                                                                                                                                                                                                        /translation="METTQTSTIASKDSRSAWRKTDTMWMLGLYGTAIGAGVLFLPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFSFNHSPIISSFAVAKREEYGDMAEQKCSKILAFAHIMMVLTVMFFVFSCVLSLTPA
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Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

(Dases 1 to 3850)

Cole.S.T. Brosch, R., Parkhill, J., Garner, T., Churcher, C.,
Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E.,
Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T.,
Connor, R., Davias, R., Devlin, K., Feltwell, T., Gentles, S.,
Hamlin, W., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A.,
Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to SDAA_ECOLI gi|1788116 percent identity 77 in 455 aa, similar to SDAB_ECOLI gi|1789161 percent identity 99 in 455 aa (Conserved in E.coli K-12)"
                                                                                                            note-"similar to SDAC_ECOLI gil1789160 percent identity 100 in 429 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD 161304 TCAATATACTACTCGTGTTTTAAAAGCGCCAAAAACCATACCACAGGAAGAAGAT 161363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 161364 ACGCCGCCCAGGTGACCAGCGCCAGCAACCACGCGACTGCATCAATAACGCGCTACCA 161423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 161424 CCAAAAATCCCCGCGCAAATCAGGACCAAATCGCTGATAGCGCAAAGTAAGGCAATCATA 161483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis H37Rv complete genome; segment 89/162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 atgccaccccagcgcataatatcgagcacgatcggcgcgggcattggacaaaagatcaacg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 tocaccttgtttgtcatggcgtctttcgctgccatgacggcaaaccataacaggtaagcg 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cccaaggtgccggcgatgaacaaaaagacgtcagaaattaaacacacgagaagaaccgca 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atgagtccttcgcgcttaattccttgtttaatcaccagtacattctgcggtccgatggac 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.7%; Score 62; DB 2; Length 266658;
11.4%; Pred. No. 2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 135; Indels
                                                                                                                                                                                                                                     /evidence=not_experimental
/product="probable serine transporter"
/protein_id="BAB37079.1"
/db_xref="GI:13363128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 agtaaaagactggcccccaaaagcagacctgtaatgaa 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
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                                                                                                                                                                                                         transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="ECs3657"
7285. .8652
5938. .7227
/gene="ECs3656"
                                                                                      /gene="ECs3656"
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Z74025.1 GI:320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local
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VERSION
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      gene
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                                                          CDS
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Jobes 1879 (MTC739.34), len: 303, LysR family member similar to many regulatory proteins, especially ICIA_ECOLI P24194, chromosome initiation inhibitor, (297 aa), and P94632 LYSTNE BYFORT REGULATOR PROTEIN. (290 aa). FASTA scores, P94632 LYSINE EXPORT REGULATOR PROTEIN opt: 705 coverlap; and ICIA_ECOLI P44194 opt: 520, z-score: 632.5, E(): 1.1e-28, (35.8% identity in 288 aa overlap; and ICIA_ECOLI P44194 opt: 520, z-score: 632.5, E(): 1.1e-28, (35.8% identity in 285 aa overlap); contains signature. Also contains helix turn-helix motif at aa 22-43, (+5.52 SD)."
                                                                                                                                                                                                                                        /db_xref="SWISS-PROT:010837"
/db_xref="SWISS-PROT:010837"
/translation="WPPRSIVRIVGVVVATTLALVSAPAGGRAAHADPCSDIAVVFAR
/translation="WPPRSIVRIVGVGGRSIGVYAVNYPASDDYRASASNGSDDASAHIOR
TYPASCPUTRIVLGGYSGGAYVIDLSTSAMPPAVADHYAVALFGEPSGFSSHIWGGG
SLPTIGPLYSSKTINLCAPDDPICTGGGNIMAHVSYVQSGMTSQAATFAANRLDHAG"
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Escherichia.
CUTI_ALTBR P41744 cutinase precursor, (209 aa) FASTA scores, opt: 283, z-score: 3220, E(): z.2e-11, (32.6% identity in193 aa overlap). Also similar to M. tuberculosis Rv3452, Rv3451, Rv2301, Rv1758, Rv3724."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctttccatttccccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gccttgctgaa----atcccgttaaccatcgccatcaacgcagattcgctatccacatgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgagtgttggtatcgcgacccaaccggccaaagcaaccgaagcgggtgaagtccttgtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6383 GCGTCGCTGAAACGCACGCGCGATCACCATTGCGGTAAACGCCCGATTCCATGGCGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6503 CAGGTGCTGGTCAGGGAAAAGCCATGTCGGGCGACGACGCCGCAGGTATCCCCGCTGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 38500;
                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Rv1984c"
/note="PSO0155 Cutinase, serine active site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                             /codon_start=1
/transl_table=11
/product="hypothetical protein Rv1984c"
/protein_id="CAA98399.1"
/db_xref="GI:1403471"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein Rv1985c"
/protein_id="CAA98410.1"
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Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 129;
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Sequence 15 from Patent EP1016710.
AX030085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(5739. .6650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="Rv1985c"
complement(5739. .6650)
/gene="Rv1985c"
                                                                                                                                                                                                                                                                                                                                                                                             complement(4950. .4967)
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55.0%;
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/gene="Rv1984c"
/note="Rv1984c, (MTCY39.35), len: 217. Probable cutinase
precursor with N-terminal signal sequence, , similarity to
                                                                                                                                                                /db_xref="SWISS-PROT:Q10840"
LATERSLAIL-LOO="WTGKLVEFKHAINWNRLLDAKDLQVWERLTGNFWLPEKIPLSND
LASPOTLSSTEQQTTIXVFTGLLLDTAQATVGAVAMIDDAYTPHEEAVLTNNAFMES
VHAKSYSSIFSTLGSTKQIDDAFDWSEQNPYLORRAQIIVDYYRGDDALKRKASSVML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MIVDTSAVVALVQGERPHATLVAAALAGAHSPVMSAPTVAECLI
VLTARHGPVARTIFERLRSEIGLSVSSFTAEHAAATQRAFLRYGKGRHRAALNFGDCM
TYATAQLGHQPLLAVGNDFPQTDLEFRGVVGYWPGVA"
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DEVSAAVAALFARFGGEYQAVSAQASAFHQQFVQTLNSASGSYAAAEATIASQLQTAQ
HDLLGAVNAPTETLLGRPLIGDGAPGTATSPNGGAGGLLYGNGGNGYSATASGVGGGA
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AAGLLGWGANGGAGGLGDGVGVDRGTGGAGGRGGLLYGGYGVSGPGGDGRTVPLEIIH
VTEPTVHANVNGGPTSTILVDTGSAGLVVSPEDVGGILGVLHMGLPTGLSISGYSGGL
                                                                                                                                                                                                                                                                             ESFLFYSGFYLPMYWSSRGKLTNTADLIRLIIRDEAVHGYYIGYKCQRGLADLTDAER
ADHREYTCELLHTLYANEIDYAHDLYDELGWTDDVLPYMRYNANKALANLGYQPAFDR
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GAVGVDGVLGVGPNAVGPGPSIPTMALPGDLNQGVLIDAPAGELVFGPNPLPAPNVEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Rv1982c, (MTCY39.37), len: 139. Similar to
Mycobacterium tuberculosis Z92772;MTY20H10_5 (131 aa)
FASTA scores: opt: 288 z-score: 388.5 E(): 4.1e-14; 40.
identityin 127 aa overlap, also similar to Rv2759c, and
Rv0609"
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/gene="PE_BGRS"
/note="PS00141 Eukaryotic and viral aspartyl proteases
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/note="ggagg, potential rbs upstream of Rv1983"
2992. .4668
/gene="PE_PGRS"
2992. .4668
/gene="PE_PGRS"
/note="Rv1983, (MTCX39.36c), len: 558; Member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1946. .1949)
/note="agga, potential rbs upstream of Rv1981c"
complement(2161. .2580)
/gene="Rv1982c"
                                                                                                                                                                                                                                                                                                                                    DTCQVNPAVRAALDPGAGENHDFFSGSGSSYVMGTHQPTTDTDWDF"
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/protein_id="cAA98401.1"
/db_xref="G1:1403473"
/db_xref="SWISS-PROT:Q10874"
     reductase small subunit signature"
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                                                                                                             /protein_id="CAA98381.1"
/db_xref="GI:1403474"
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/protein_id="CAA98400.1"
/db_xref="G1:1403472"
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/gene="Rv1982c"
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                                                                                                                                                                                                                                                                           /protein_id="CaO09317.1"
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/db_xref="G1:10190303"
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FGLALLAAWLAPRLRTAKAQRIINLYVGCVWWFIALQLARDGIAHAQALFS"
- 143 c 180 g 193 t
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Submitted (22-FEB-1989) Alefounder P.R., University of Cambridge, Department of Chemistry, Lensfield Road, Cambridge CB2 1EW, England 2 (bases 4376 to 5508)
Alefounder, P.R., Baldwin, S.A., Perham, R.N. and Short, N.J. Cloning, sequence analysis and over-expression of the gene for the class II fructose 1,6-bisphosphate aldolase of Escherichia coli
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1 (bases 1 to 636)
Nakanishi,K., Aleshin,V.V., Livshits,V.A., Tokhmakova,I.L.,
Troshin,P.V. and Zaskatewey,N.P.
Wethod for producing 1-amino acids
Patent: EP 1016710-A 15 05-JUL-2000;
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Escherichia coli fda, pgk and gapB genes for fructose
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X14436 X141417
fda gene; fructose 1,6 biphosphate aldolase; gapB ge
glyceraldehyde 3-phosphate dehydrogenase; pgk gene;
phosphoglycerate kinase; unidentified reading frame.
Escherichia coli.
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Pred. No. 2.2e-07;
0; Mismatches 136;
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                                                                                                                     1. 636
/organism="Escherichia coli"
/db_xref="taxon:562"
1. 636
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/db_xref="SWISS-PROT:P21437"
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ERLISRKIAGGLTRQVAEAFYARTDGPNVERVLMNSRQANLIVEMTEEGRYHFTS"
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TVAFR
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-339)"
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  Biochem. J. 257 (2), 529-534 (1989)
89193446
Data kindly reviewed (28-JUN-1989) by Alefounder P.
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J. 257 (2), 529-534 (1989)
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Length 8029;

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Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-071-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA This sequence was determined by the E. coll Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director) Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coll K12 strain MG1655. Predicted open reading frames were determined using Genemark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                              7006 CCAAAAATCCCGGCGCAAATCAGGACCAAATCGCTGATAGCACAAAGTAAGGCAATCATA 6947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6946 ATGTGGTACTGACGACGTATGCCCTGATTCATCACAAAAGCATTTTGTGGACCGAGCGGT 6887
                                                                                                                                                                                                                                                                                                                                                                                                                                      atgagtcettcgcgettaatteettgtttaatcaccagtacattctgcggtccgatggac 288
                                                                                                                                                                                                                                109 atgccaccccagcgcataatatcgagcacgatcggcgcggcattggacaaaagatcaacg 168
                                                                                                                              49 tecacettgtttgtcatggcgtctttcgctgccatgacggcaaaccataacaggtaagcg 108
                                                                                                                                                                                                                                                             169 cccaaggtgccggcgatgaacaaaaagacgtcagaaattaaacacacgagaagaaccgca
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                                                                            0; Mismatches 136;
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                          DB 2;
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Escherichia coli K12 MG1655 section 265
                          Score 60.4; DB 2
Pred. No. 3.8e-07
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Blattner,F.R., Plunkett,G. I
Riley,M., Collado-Vides,J.,
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Blattner, F. R.
Direct Submission
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Blattner, F.R.
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Escherichia coli K12
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Submitted (02-SEP-
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1922 c 2114 g 2009 t
                                                                                                                                                                           /translation="MSVIKMTDLDLAGKRVFIRADLNVPVKDGKVTSDARIRASLPTI
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                                                                                                                                                                                                                             EGELVVLENVRFNKGEKKDDETLSKKYAALCDVFVMDAFGTAHRAQASTHGIGKFADV
                                                                                                                                                                                                                                                          ACAGPLLAAELDALGKALKEPARPMVAIVGGSKVSTKLTVLDSLSKIADQLIVGGGIA
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RVIVGVNKYKLDHEDETDVLEIDNVMVRNEQIASLERIRATRDDAAVTAALNALTHAA
PURBELLABAVNAARVRATLGEISDALEVAPORYVEVPEQGVYGVIAQSYHQERESASE
PDAIVAQTEQELABOKRRPRILIARMGODGHDRGARVIASAVSDLGFDVDLSPMFSTP
EEIRRLAVENDVHVVGASSLAAGHKTLIPELVEALKKWGREDICVVAGGVIPPQDYAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETEVARMVDCFISLOIAGGDDLOGIKKGLMEVADLIVINKDDGDNITNVAIARHMYE
SALHILRRKYDEWQPRVLTCSALEKRGIDEIWHAIIDFKTALTASGRLQQVRQQQSVE
WLRKQTEEEVLNHLFANEDFDRYYRQTLLAVKNNTLSPRTGLRQLSEFIQTGYFD"
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VIPPFMYFSTVLQESVVHLLETGKISGASASSITISADSLRKIYDNMDYFASRIVLRP
QIESNNPETIRRLGVIALNYGLEFDISGASSITISADSLLKKIYDNMDYFASRIVLRP
FMAPSIAKEGKISTVPVPMCSHVDHSHSVKVIITEGGIADLAGLSPLQRARTIIDNCA
HPMYRDYLHRYLENAPGGHIHHDLSHVFDLHRNLIATGSMLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DA IMPYCGNTLRLGVTGTPGAGKSTFLEAFGMLLIREGLKVAVIAVDPSSPVTGGSIL
GDKTRMNDLARAEAAFIRPVPSSGHLGGASQRARELMLLCEAAGYDVVIVETVGVGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFTDDLMQALSDLNRPEIRCITLRAPSGSKVFSAGHDIHELPSGGRDELSYDDPLRQI
TRADQKFPK PIISMVGGSVWGGAFEMIMSSDLITAASTSTESWIPVNLGVPYNLVGIH
NLTRDAGFHUVKELIFTASPITATORALLAVGILNHVVRYEELEDFTLOMAHHISRKAPL
AIAVIKEELRVLGEAHTMNSDEFRIQGMRRAVYDSEDYQEGMNAFLEKRKPNFVGH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANEQHEAKKPYQIRLLIGASISAAADDVLSDADAVSWRAPYQTSSGLRKKINQGAVSF
VDLHLSEVAQMVNYGFFGDIDVAVIEASALAPDGRVWLTSGIGNAPTWLLRAKKVIIE
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                        AGSYYIESLTDQIVKQARAIIQQIDEAGGMAKAIEAGLPKRMIEEASAREQSLIDQGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MNLSRRNILIKGIFMSYQYVNVVTINKVAVIEFNYGRKLNALSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="putative enzyme; Not classified"
/note="0275; This 275 aa ORF is 30 pct identical (6 gaps)
to 250 residues of an approx, 296 aa protein ECHW_RAT SW:
p14604"
                                                                                                                                                                                                                                                                                                          3335. .4330
//gene="ygfD"
/function="phenotype; Not classified"
/note="0331; 100 pct identical to YGFD_ECOLI SW:
P27254(257 aa) but has 25 additional N-ter aa 50 additional C-ter aa; orf2 of X66836"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"putative nucleotide-binding protein"
/protein_id="AAC75955.1"
/db_xref="GI:1789285"
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/protein_id="AAC75957.1"
/db_xref="GI:1789287"
                                                                                                                                                                                  LQERGVAAIYGPGTPMLDSVRDVLNLISQHHD"
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/product="putative enzyme"
/protein_id="AAC75956.1"
/db_xref="G1:1789286"
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/gene="ygf1"
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/transl_table=11
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5150. .6628
/gene="ygfH"
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3335, .4330
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/gene="ygfH"
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/gene="ygfD"
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/gene="ygfG"
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/gene="ygfG"
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30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic by Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coli KIZ sequence and
                                                                                                                                                                                                                                                                                                                                         (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monicased products; all new functional assignments courtesy of Monicasequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEGOPILVREVPPRETEDGOKILALIRQVELLEEEWIGDEOTGSTPILLISLANNADSI.
ATWILPALAPVLADSPIRLNLQVEDETRTQERLREEVGGOVSTQHOALPSCLVDKLG
ALDYLEVSSKPFAEKYFPNGVTRSALLKAPVVAFDHLDDMHQAFLQQNFDLPPGSVPC
HIVNSSEAFVQLARQGTTCCMIPHLQIEKELASGELIDLTPGLFQRRMLYWHRFAPES
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DNLEVTGTLPGLPPYVRGPRATMYTAQPWTIRQYAGFSTAKESNAFYRRNLAAGQKGL
SVAFDLATHRGYDSDNPRVAGDVGKAGVAIDTVEDMKVLFDQIPLDKMSVSMTMNGAV
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FGIGMDLFMNVAMLRAARYLWSEAVSGFGAQDPKSLALRTHCQTSGWSLTEQDPYNNV
IRTTIEALAATLGGTQSLHTNAFDEALGLPTDFSARIARNTQIIIQEESELCRTVDPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MKRPDYRTLQALDAVIRERGFERAAQKLCITQSAVSQRIKQLEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'function="enzyme; Degradation of small molecules: Fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="0714; 99 pct identical to SBM_ECOLI SW: P27253"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="factor Sigma70; predicted +1 start at 3058751"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(9. .40)
/note="factor Sigma70; predicted +1 start at 3057674"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="factor Sigma70; predicted +1 start at 3057742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="replication initiation inhibitor, binds to 13-mers at oric"
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/protein_id="AAC75954.1"
/db_xref="GI:1789284"
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/db_xref="GI:1789283"
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complement(9. .40)
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/transl_table=11
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/gene="iciA"
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/gene="iciA"
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/gene="sbm"
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'qene="sbm"
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AKRVXĶLKNANRFFVASDVHPOTLDVVRTRAETFGFEVIVDDAOKVLDHQDVFGVLLQ
QVGTTGEIHDYTALISELKSRKIVVSVAADIMALVLLTAPGKQGADIVFGSAQRFGVP
MGYGGPHAAFFAAKDEYKRSMGRIIGVSKDAANTALRAMAMOTREQHIRREKANSNI
CTSQVLLANAIASLYAVYHGPVGLKRINAINLINDILAAGLQQKGLKLRHAHYFDTLC
VEVADKAGVLTRAEABINLARDILANGITLLDETTTRENVQLFNVLLGDNHGLDID
TLDKDVAHDSRSIQPAMLRDDEILTHPVFNRYHSETEMMRYMHSLERKDLALNQAMIP
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YFTEDFFRLVVNSATREKDLSWITQHAEPFGIEITVRDDLSMIAVOGPNAQAKAATLF
NDAQRQAVEGMKPFFGVQAGDLFIATTGYTGEAGYEIALPNEKAADFWRALVEAGVKP
                                                                                                                                               /translation="MAIALVTGGSRGIGRATALLLAQEGYTVAVNYQQNLHAAQEVMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="WTQTLSQLENSGAFIERHIGPDAAQQQEMLNAVGAQSLNALTGQ
IVPKDIQLATPPQVGAPATEYAALAELKAIASRNKRFTSYIGMGYTAVQLPPVILRNM
LENPGWYTAYTPYQPEVSQGRLEALLNFQQVTLDLTGLDMASASLLDEATAAAEAMAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGSCTWKLNAAAEMIPITWPEFAELHPFCPPEQAEGYQOMIAQLADMLVKLTGYDAVC
MODSGAGEFYAGLLAIRHBENREGHBJOLLPASAHGYNESAHMAGMOVVVVAC
MKONIDLTDLRAREQAGDMLSCIMVTYPSTHGVYEFTIREVCEVVHOFGGOYTLDG
ANMNAQVGITSPGFIGADVSHLNLHKTFCIPHGGGFGMGPIGVKAHLAPFVPGHSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MSNVPAELKYSKEHEWLRKEADGTYTVGITEHAQELLGDMVFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPEVGATVSAGDDCAVAESVKAASDIYAPVSGEIVAVNDALSDSPELVNSEPYAGGWI
FKIKASDESELESLLDATAYEALLEDE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGLGARDTERLEAGMNLYGOEMDETISPLAANMGWTIAWEPADRDFIGREALEVQREH
GTEKLVGLVMTEKGVLRNELPVRFTDAQGNQHEGIITSGTFSPTLGYSIALARVPEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QIEGMLTRQGAVSAAPFGSASILPISWMYIRMGAEGLKKASQVAILNANYIASRLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFPVLYTGRDGRVAHECILDIRPLKEETGISELDIAKRLIDYGFHAPTMSFPVAGTLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEPTESESKVELDRFIDAMLAIRAEIDQVKAGVWPLEDNPLVNAPHIQSELVAEWAHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MAQQTPLYEQHTLCGARMVDFHGWMMPLHYGSQIDEHHAVRTDA
                                                                                                                                                                                                                                                                                                                                                                        complement(318. .3634)
//note="similar to Genbank Accession Number L20872" (ECGCCWHP); bases 3318 to 3438 differ from the sequence presented here, as well as from X73958 and D21144"
                                                                                                                                                                         LITQAGGKAFVLQADISDENQVVAMFTAIDQHDEPLAALVNNAGILFTQCTVE
                                                                                                                                                                                                       complement(1. .5335)
note="similar to GenBank Accession Number X73958
                                                                                                                                                                                                                                                                                                                      /note="similar to GenBank Accession Number D21144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(3809. .5631)
/note="similar to GenBank Accession Number M97263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSREVAVFPAGVADKYWPTVKRLDDVYGDRNLFCSCVPISEYQ'
                                                                                /protein_id="AAA69070.1"
/db_xref="G1:882432"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAA69071.1"
/db_xref="GI:882433"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAA69072.1"
/db_xref="G1:882434"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3551. .3940)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(559. .3432)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3432)
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                                                           /transl_table=11
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/note="ORF_f129"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                          complement(1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="gcvP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="gcvP'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="gcvH"
                                                                                                                                                                                                                                                                                                                                                   (ECOPYU18)
                                                                                                                                                                                                                                                             (ECGCVOP)
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/function="putative regulator; Not classified"
/note="f303; This 303 aa ORF is 25 pct identical (11 gaps)
to 241 residues of an approx. 304 aa protein CYNR_ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-JUN-1995) Guy Plunkett, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA This sequence was determined as part of the E. coli Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Frederick R. Blattner, director) at the University of Wisconsin-Madison. Supported by award HG00301 from the NIH Human Genome Project. The entire sequence was independently determined from E. coli MG1655, overlaps with other sequence determinations are annotated. This entry should be considered somewhat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               provisional; it will be updated and merged with others at a later
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
1 (bases 1 to 87107)
                                                                                                                                                                       /product="putative transcriptional regulator LYSR-type"
/protein_id="AaC75958.1"
/db_xref="GI:1789288"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8867 TCAATATTACTGCTCATTGCTGTTTTAAAAGCGCCCAAAACCATACCACAGCAAGAAGGCT 8926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 atgccaccccagcgcataatatcgagcacgatcggcggcggcattggacaaaagatcaacg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 atgagtocttcgcgcttaattccttgtttaatcaccagtacattctgcggtccgatggac 288
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68 minutes.
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                                                                                                                                                                                                                                                                                     Length 10362;
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/map="approximately 65 to 68 minutes"
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                                                                                                                                                                                                                                                                                                                                              0; Mismatches 136;
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                                                                                                                                                                                                                                                                                     Score 60.4; DB 1;
Pred. No. 4.1e-07;
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                                                                                                                                                  /transl_table=11
                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                     Query Match 8.5%;
Best Local Similarity 51.1%;
Matches 142; Conservative
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                                                                                      SW:
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Best Local Similarity
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AUTHORS
TITLE
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/translation="msaqpvdiqifgRSLRvNCPPDQRDalnqaadDLNQRLQDLKER
TRVTNTEQLVFIAALNISYELAQEKAKTRDYAASMEQRIRMLQQTIEQALLEQGRITE
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                                                                                                                                                                                                                                                                                           /product="stable 6S RNA"
10374. .10556
/gene="ssr"
10374. .10557
/none="similar to GenBank Accession Number X01238
(ECRRN6S)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 atgccaccccagcgcataatatcgagcacgatcggcgcgggcattggacaaaagatcaacg
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                                                                                                                                                                                10266. .11219
/note="similar to GenBank Accession Number M12965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 60.4; DB 2; Length 141744; 51.1%; Pred. No. 7.1e-07; ve 0; Mismatches 136; Indels 0;
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Job time: 15035 sec
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                                                                                                                                                                                                                                                             10374. 10556
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                                                                                                                                                                                     misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="msv1IVGGGMaCaTLaLaISRLSHGALPVHLIEATAPESHAHPGFDGRAIALAAGTCQQLARIGVWQSLADCATAITTVHVSDRGHAGFVTLAAEDYQLAAL
GQVVELHNVGQRLFALLRRAPGVTLHCPDRVANVARTQSHVEVTLESGETLTGRVLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCSLVWCHPLERREEVLSWSDEKFCRELQSAFGWRLGKITHAGKRSAYPLALTHAARS
ITHRTVLVGNAAQTLHPIAGGGFNLGMRDVMSLAETLTQAQERGEDMGDYGVLCRYQQ
RRQSDREATIGVTDSLVHLFANRWAPLVVGRNIGLMTMELFTPARDVLAQRTLGWVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /traislation="MSEISROBEQRRRQALVEQMOPGSAALIFAAPEVTRSADSEYPY
RONSDFWYFTGFNEPEAVLY/LIKSDDTHNHSYLFNRRVRDITAEIWFGRRLGODAAPEK
RONSDFWYFTGFNEPEAVLY/LIKSDDTHNHSYLFNRRYRDITAEIWFGRRLGODAAPEK
ATM DWRPVYHEMELEKSPEELAYLRRAGEITAMAHTRAMEKCRPGMFEYHLEGEIHH
EFNRHGARYPSYNTIVGSGENGCILHYTENECEMRDGDLYLIDAGCEYKGYAGDITRT
                                                                                                                                                                                                                                                                                                                                                                                                                     IGADGANSWLRNKADIPLIFWDYQHHALVATIRTEEPHDAVARQVFHGEGILAFLPLS
PHLCSILWASLSPEEAQRWQASEDEENRALMA REDNRACIGCKVESAROYPPLIGRYA
RQFRSHRLALVGDAHTIHPLAGGGVNLGFWDAAELIAELKRLHRGRYDIGYIYLRR
YERSRKHSAALMLAGWQGFRDLFSGTNPAKKLLRDIGLKLADTLPGVRPQLIRQAMGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPVNGKFTQAQREIYDIVLESLETSLRLYRPGTSILEVTGEVVRIMVSGLVKLGILKG
DVDELIAQNAHRPFFWHGLSHWLGLDVHDVGVYGQDRSRILEPGMVLTVEPGLYIAPD
AEVPEQYRGIGIRIEDDIVITETGNENLTASVVKRPEEIEALMVAARKQ"
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DSSWLPLLTNEGMAFGFELQALKKHGSATSDALQDDGFLFQLYLDGGDDVSVFD
RADALAGWVNHFLLGLGVTQPRLDKVTGETGEATDDLRNIAQLGYDEDEDQEELEMSL
EBIIEDYRNYAALLCHDFFTHPQPTAPEDVQKPTLH"
                                                                                                                                                                                                                                                                                                                                                                   PPQLRVSAINAASEKLLTRLGVWQDILSRRASCYHGMEVWDKDSFGHISFDDQSMGYS
HLGHIVENSVIHYALWNKAHQSSDITLLAPAELQQVAWGENETFLFLKDGSMLTARLV
                                                                                                                                                                                                                                                                                                                                             /translation="MQSVDVAIVGGGMVGLAVACGLQGSGLRVAVLEQRVQEPLAANA
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                                                 'note="similar to GenBank Accession Number D90281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note-"ORF_f441; third start codon"
GETAIVQIRNREMPVKVTKPVFVRNGKAVA"
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/protein_id="AAA69076.1"
/db_xref="G1:882438"
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/protein_id="AAA69074.1"
/db_xref="G1:882436"
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/protein_id="AAA69075.1"
/db_xref="G1:882437"
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/db_xref="G1:882439"
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                                                                                                complement(5506. .6708)
                        complement(5370.
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourle and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.9%; Score 63.2; DB 1; Length 1
55.3%; Pred. No. 3.3e-10;
tive 0; Mismatches 128; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/390,878
FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
US-08-438-862-4
US-09-124-671-24
US-09-001-982-11
US-09-001-982-11
US-09-076-193-6
US-08-073-303-3
US-08-073-303-5
US-09-073-303-3
US-09-073-303-5
US-09-126-280-1
US-09-126-280-1
US-09-126-280-1
US-09-126-280-1
US-09-126-280-1
US-09-126-280-1
US-09-126-280-1
US-09-126-280-1
US-09-126-280-1
US-09-126-155-16
US-09-128-155-16
US-09-128-155-16
US-08-685-653-1
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REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15371A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/08390878; Patent No. 5700683; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415/543/5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15239 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELEPHONE: 415/543/9600
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Matches 166; Conservative
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11970
152331
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176373
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2635
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STATE: California
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                                                                                                                                           time 93.36 Seconds
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/cgnl_7/ptodata/1/ina/5B_COMB.seq:*
/cgnl_7/ptodata/1/ina/6A_COMB.seq:*
/cgnl_7/ptodata/1/ina/6B_COMB.seq:*
/cgnl_7/ptodata/1/ina/PcTuS_COMB.seq:*
/cgnl_7/ptodata/1/ina/PcTuS_COMB.seq:*
                     4.5
Compugen Ltd.
                                                                                                                                     September 14, 2001, 04:24:46; Search (without 1441.733
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US-08-388-353-800
US-08-488-551B-800
US-07-867-194-3
US-07-867-194-4
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US-09-266 417-33
US-08-078-271B-9
US-09-150-460B-9
US-08-232-463-14
US-09-385-028-21
US-09-385-028-21
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US-08-685-625A-5
US-08-714-918-33
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US-08-438-863-4
                                                                                                                                                                                                                                                                                                                                                                     324599 segs, 94655562 residues
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                       GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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11604
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Maximum DB
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                                                                                                                                           Run on:
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538 cgagtgttggtatcgcgcacc
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US-08-470-588-1/c
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                                                                                                                  5373 CAGGTGCTGGTGGTCAGGAAAAGCCATGTCGGGCGACGACGCAGGTATCCCGCTGTTG 5432
                                                                                                                                                                                                                                                                    5493 GCGTCGCTGAAACGCACGCGGATCACCATTGCGGTAAACGCCGATTCCATGGCGGACATGG 5552
478 ctttccatttccccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kaphammer, Bryan J.
TITLE OF INVENTION: tfdA Gene Selectable Markers in Plants and the
TITLE OF INVENTION: Use Thereof
                                      5313 CTACATGTCACCCCTCGGCTGTCAGTCAGCGCATCAAGTCGTTGGAGCAGCAGGTCGGC
                                                                                                                                                              598 caagcagcgggaaaatggtgttgctgcaagcagaaactaaagcgcaactatctgg--ac
                                                                                                                                                                                                                                             656 gccttgctgaa----atcccgttaaccatcgccatcaacgcagattcgctatccacatgg
                                                                                538 cgagtgttggtatcgcgcacccaaccggccaaagcaaccgaagcgggtgaagtccttgtg
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Pred. No. 0.035;
0; Mismatches 65; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANUKESSEE: Sterne, Ressler, Goldstein & Fox STREET: 1100 New York Avenue, Suite 600 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1405.0030001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,117
FILLING DATE: 15-DEC-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                             US-08-358-117-1/c
Sequence 1, Application US/08358117
Patent No. 5608147
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: 1: LENGTH: 2058 harry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.2%;
Best Local Similarity 53.9%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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751..1611
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LOCATION:
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2,4-DICHLOROPHENOXYACETIC ACID (2,4-D) MONOOXYGENASE FORMATION AND PROCESS FOR THE PRODUCTION OF THESE PLASMIDS AND STRAINS
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Pred. No. 0.035;
0; Mismatches 65; Indels
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                                                                                                                                                                                                                                                                                                                 E: FROMMER LAWRENCE & HAUG LLP
745 FIFTH AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995
07-JUN-1995
07-JUN-1995
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APPLICATION NUMBER: US/OR///TTRIEFING
                                                                                                                                                                                                          MICROORGANISMS
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                                                                                                                                GENERAL INFORMATION:
APPLICANT: STREBER, WOLFGANG R.
APPLICANT: TIMMIS, KENNETH N.
APPLICANT: ZENK, MEINHART H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: LAWRENCE, WILLIAM F.
REGISTRATION NUMBER: 28,029
REFERENCE/DOCKET NUMBER: 5144
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEPASX: 212-588-0500
410 GTGTTGTTGTTCGAGCGCAGC 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.2%;
Best Local Similarity 53.9%;
Matches 76; Conservative
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LENGTH: 2058 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                  TITLE OF INVENTION: MITTITLE OF INVENTION: 2
TITLE OF INVENTION: F
TITLE OF INVENTION: F
TITLE OF SEQUENCES: A
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292 aaaagactggcccccaaaagcagacctgtaatgaagatttccatgatcaccatcgtgacc 351
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48.3%; Pred. No. 0.77;
ive 7; Mismatches 68; Indels 0
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Patent No. 6187541
GENERAL INFORMATION:
APPLICANT: Benton, Bret
APPLICANT: Malouin, Francois
APPLICANT: Malouin, Francois
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILLING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILLING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222/005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 222/
RELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 6-3510
INFORMATION FOR SEQ ID NO: 33:
                 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
TYPE: nucleic acid
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Best Local Similarity 48.3
Matches 70; Conservative
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  CORRESPONDENCE ADDRESS
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US-08-714-918-33
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US-09-265-315-33
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    GENERAL INCUMENTION:
APPLICANT: UBNO, Nacto
APPLICANT: UBNO, Nacto
APPLICANT: MATSUMOTO, Kunihiro
APPLICANT: MATSUMOTO, Kunihiro
APPLICANT: TRIE, Kenji
TITLE OF INVERTION: NOVEL KINASE IN TGF-BETA FAMILY SIGNAL
TITLE OF INVERTION: TRANSDUCTION SYSTEM
NUMBER OF SEQUENCES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
LIP: 22313-1404
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,625A
FILING DATE: 29-SEP-1995
ATTORNEY APPLICATION NUMBER: US/08/685,6267
FILING DATE: 29-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
RECISTRATION NUMBER: 001560-267
TELECOMMUNICATION INFORMATION:
TELEPRAN: (703) 836-620
TELECOMMUNICATION INFORMATION:
TELEPRAN: (703) 836-620
TELENGTH: A056 DASE PAILS
SEQUENCE CHARACTERISTICS:
LENGTH: A056 DASE PAILS
SEQUENCE CHARACTERISTICS:
LENGTH: A056 DASE PAILS
WUDE: NUMBER: A016
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| Patent No. 6037123 | Application US/08714918
| GENERAL INFORMATION: APPLICANT: Benton, Bret | APPLICANT: Lee, Ving APPLICANT: Malouin, Francois APPLICANT: Malouin, Francois APPLICANT: Schnid, Molly B. APPLICANT: Schnid, Molly B. APPLICANT: Schnid, Molly B. TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL TITLE OF INVENTION: TARGET GENES | NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 2656;
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Pred. No. 0.79;
0; Mismatches
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Best Local Similarity 63.0%;
Matches 51; Conservative
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STRANDEDNESS: double
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GENERAL INFORMATION:
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US-08-685-625A-5
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292 aaaagactggcccccaaaagcagacctgtaatgaagatttccatgatcaccatcgtgacc 351
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APPLICANT: Malouin, Francois
APPLICANT: Matouin, Francois
APPLICANT: Schmid, Molly B.
APPLICANT: Schmid, Molly B.
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.6%; Score 32.8; D:
Best Local Similarity 48.3%; Pred. No. 0.77
Matches 70; Conservative 7; Mismatches
                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION A 435
PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTONEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/COCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELERAX: (7.31) 955-0440
ITELER A7.3510
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412 cccattcaactggacactttgctct 436
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                                                   Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1876 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
     CORRESPONDENCE ADDRESS
                            ADDRESSEE: Lyon & I
STREET: 633 West Fi
STREET: Suite 4700
                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-266-417-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 tatggaagtacttaagtaaaatgattggttcttaacatggtttaatatagcttcatgaac 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            666 AATGGTTTGAGATATKTCGACAGTTTGGTTWTTTACCTGGATTTATATTGTTATATTA 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Malouin, Francois
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
4.6%; Score 32.8; DB 4;
Best Local Similarity 48.3%; Pred. No. 0.77;
Matches 70; Conservative 7; Mismatches 68;
                                                                                                                   COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPREATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        726 GAGCINTAATTCCAGTATTCCTTT 750
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Patent No. 6187541
GENERAL INFORMATION:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS: LENGTH: 1876 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY:
US-09-265-315-33
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Length 1876; Indels

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165 aacgeecaaggtgeeggegatgaacaaaaagaegteagaaattaaacacaegagaagaae 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 ACCGGACATGTCAAGAACGGGACGATGAGGATCGTCGGTCCTAAGACCTGCAGGAACATG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 AGGGGGGCCTGGCGAGGGGACGGCATCATGCACACTCGCTGCTGTGGAGCTGAGATC 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalian Circadian Rhythym-Like Gene
                                                                                                                                         Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31.2; DB Pred. No. 0.85; 0; Mismatches
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Patent No. 6190882
GENERAL INFORMATION:
APPLICANT: Lee, Cheng-Chi
APPLICANT: Bencht, Urs
APPLICANT: Bichele, Gregor
APPLICANT: Bun, Zhong Sheng
TILE REFERENCE: D6039
CURRENT APPLICATION NUMBER: US/09/150,460B
CURRENT FILING DATE: 1998-09-09
PRIOR FILING DATE: 1997-09-09
                                                                                                                                                                                                                                                 CLASSIFICATION DATE:

CLASSIFICATION NUMBER: US/08/078,271B
FILING DATE: 15-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE91/01020
APPLICATION NUMBER: DE 40 41 304.7
FILING DATE: 20-DEC-1991
PRIOR APPLICATION NUMBER: DE 40 41 304.7
FILING DATE: 21-DEC-1990
ATTORNEY AGENT INFORMATION:
NAME: Hanson, No. 6136527man D.
REGISTRATION UNMER: ALGER 201
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 688-9200
TELEFAX: (212) 688-9200
TELEFAX: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 cgcaatgagtccttcgcgcttaattcct 252
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: 805 Third Avenue
New York City
New York
                                                                                                                                                                                       PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 219 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                          Wordperfect
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 75; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 9
                                                                                                                                                                                     OPERATING SYSTEM:
                                             STATE: New COUNTRY: US. ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-150-460B-9
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Sequence 9, Application US/08078271B
Patent No. 6136527
GENERAL INFORMATION:
APPLICANT: Fuchs, Klaus; Motz, Manfred; Roggendorf, Michael;
APPLICANT: Soutschek, Erwin
TITLE OF INVENTION: Polypeptides Derived from Proteins of the
TITLE OF INVENTION: Hepatitis C Virus, Test Kits Containing these Polypeptides
TITLE OF INVENTION: and Vaccines against Infection by Hepatitis C Virus
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 aaaagactggcccccaaaagcagacctgtaatgaagatttccatgatcaccatcgtgacc 351
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Pred. No. 0.77;
7; Mismatches 68; Indels 0
                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,417
FILING DATE: March 9, 1999
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: MARCH 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 06/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 66/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/248
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         412 cccattcaactggacactttgctct 436
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                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 4.6%;
Best Local Similarity 48.3%;
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1876 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                 CITY: Los Angeles
STATE: California
                                                                                                                                                               COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-078-271B-9
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Query Match
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              Nucleotide sequence of m-rigui, a murine brain cDNA homologous to a human RIGUI 4.7 cDNA probe
                                                                                                                                                                            451 ggcagcttcgaaggcgcctccttagccctttccatttccccctcggcggtgagtcagcgc 510
                                                                                                                                                                                                                                                   511 gttaaagctctcgagcatcacgtgggtcgagtgttggtatcgcgccccaaccggccaaa 570
                                                                                                                                              Gaps
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                                                                                                       DB 4; Length 4700;
                                                                                                     Score 31; DB 4; Length 470
Pred. No. 4.7;
0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                             571 gcaaccgaagcgggtgaagtccttgtgcaagcagcggg 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALUNESSEE: Foley & Lardner STREE: 1800 Diagonal Road, Suite 500 STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29,768
                                                                                                       4.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7218 base pairs
                                                                                                                      Best Local Similarity 49.79
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 7218 base pai
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
             ) OTHER INFORMATION:
) OTHER INFORMATION:
US-09-150-460B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-232-463-14/c
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                                                                                                       Query Match
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1070 RRRRATCGCAAGCTCCCTCGACCTGCAGCTCGGAATTAATTCTGTGAGCGTATGG 1011
                                                                                                                                  84 gacggcaaaccataacaggtaagcgatgccaccccagcgcataatatcgagcacgatcgg 143
                                                                                                                                                                                                   144 cgcggcattggacaaaagatcaacgcccaaggtgccggcgatgaacaaaaagacgtcaga 203
                                                                                                                                                                                                                                                                                                  204 aattaaacacacgagaagaaccgcaatgagtccttcgcgcttaattccttgtttaatcac 263
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APPLICANT: CAMERON, Beatrice
APPLICANT: CROUZET,
APPLICANT: CROUZET,
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF RECOMBINANT
TITLE OF INVENTION: PROTEINS, PLASMIDS AND MODIFIED CELLS
4.4%; Score 31; DB 1; Length 7218; 14.2%; Pred. No. 5.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                                                   Conservative 140; Mismatches 175;
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STREET: 500 Arcola Road, Mailstop 3C43
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REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST94069-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,900
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: WO PCT/FR95/
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: FR 94/11049
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08793900
Patent No. 6143518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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CORRESPONDENCE ADDRESS:
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                    Best Local Similarity
Matches 52; Conserve
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                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                    ;
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                                                                                                                                                        Length 8501;
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STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                    Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Petnetin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
                                                                                                                                                                                                    57;
                                                                                                                                                          Score 30.8; DB 3;
Pred. No. 7.4;
0; Mismatches 57;
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CLASSIPLCATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-5AN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. DOUGLAS PTICE
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P5745
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 538 -666
TELEFROM: (202) 39305350
TELEFROM: (202) 39305350
TELER: RCA 24853 IDEA UR
: INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF INVENTION: Acid Biosynthesis R OF SEQUENCES: 25
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Patent No. 6232106
GENERAL INFORMATION:
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APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: DNA (genomic) US-09-385-028-21
                                                                                                                                                          Query Match 4.3%;
Best Local Similarity 53.3%;
Matches 65; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
8501 base pairs
                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
NOLECULE TYPE: CDNA
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COMPUTER READABLE FORM:
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                                                                                               449 aaggcagcttcgaaggcgcctccttagccctttccatttccccctcggcggtgagtcagc 508
                                                                                                                                           284 ACGGCAGCATCAACCGGGCCGCGGGGGTGTTCGATCAGCCAGTCGGCGCTCACCCGCC 225
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                                                   Gaps
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                                                                                                                                                                                                                  509 gcgttaaagctctcgagcatcacgtgggtcgagtgttggtatcgcgcacccaaccgg 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
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Length 1299;
                                              54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC STREET: The Jenifer Buliding, 400 Seventh Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
Score 30.6; DB 4;
Pred. No. 3.3;
0; Mismatches 54;
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Best Local Similarity 53.8%; Pred. No. 10;
Matches 63; Conservative 0; Mismatches
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. DOUGLAS Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452
                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/09385028 Patent No. 6232106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
TELERA: (202) 39305350
TELEX: CCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: DNA (genomic)
US-09-385-028-13
  4.3%;
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Susan E. Jensen
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  Query Match 4.3
Best Local Similarity 53.8
Matches 63; Conservative
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US-09-385-028-13/C
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        Query Match
        4.3%;
        Score 30.6;
        DB 4;
        Length 15079;

        Best Local Similarity
        53.8%;
        Pred. No. 11;
        Dred. No. 11;
        Dred. No. 11;

        Matches
        63;
        Conservative
        0;
        Mismatches
        54;
        Indels
        0;
        Gaps
        0;

        Qy
        449
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        568
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Search completed: September 14, 2001, 07:51:13

Job time: 12387 sec

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qb_est28:*;

qb_est29:*;

db_est31:*;

qb_est31:*;

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  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                         10228115 seqs, 4726426750 residues
                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                           US-09-105-117I-1_COPY_1016_1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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| 117; gp_est48;*
| 118; gp_est48;*
| 119; gp_est50;*
| 120; gp_est51;*
| 121; gp_est51;*
| 122; gp_est51;*
| 123; gp_est51;*
| 124; gp_est51;*
| 125; gp_est55;*
| 126; gp_est55;*
| 137; gp_est61;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.

JOURNAL Submitted (28-MAR-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr) REFERENCE 2 (bases 1 to 330) AUTHORS ROth.C.W., Brev.P.T., Ke.Z., Collins,F.H. and Weissenbach,J.	Direct Submission Submitted (28-MAR-2001) BBMI, Institut Pas Roux, Paris 75015, France This clone is from an A. gambiae BAC libra Collins and sequenced by Genoscope in coll Laboratory of Biochem. and Biol. Molec. of	FEATURES Pasteur. 1. 830 1830 Actain="pasteur" Actain="pasteur	8.5%; Score 60.4; servative 50.7%; pred. No. 8.5 nservative 1; Mismatches accttgtttgtcatggggtctttgctg		A STATE OF THE STA	NETRIE DISCOURCE ORGANISM PLASMID Drosophila melanogaster ORGANISM Plasmid Drosophila melanogaster ORGANISM Plasmid Drosophila Mithropoda Arthropoda Arthropoda Arthropoda Arthropoda Bukaryota; Meazaca Arthropoda Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. REFERENCE 1 (bases 1 to 916) AUTHORS Genoscope. TITLE Direct Submission JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
Description	Anophe Drosop 601810 Tetrao	A1020087 ubl4cd4.r A1174155 vz84d11.r AL104520 Drosophil AQ405681 HS_5076_A BR485823 a19875.5 AW351850 RC1-CT019 BR352878 IL3-HT061 AQ851405 LMAJFV1_1 AW067177 683016G08 AZ553065 RPC1-23-9	AQ782619 HS_3183_B AQ991044 REC01899 BF269985 GA_ED000 AZ834870 ZM0117K13 AAZ834861 ZM0117I15 AV706549 AV706549 BB565230 BB565230 AAR79865 W01a11.r AA794877 vv64411.r A1315494 uj51007.y	AA497438 vh28d07.r BE290613 601088315 AA065568 m171c07.r AL477555 T. brucei BF01664 uy34a01.y BE3303625 601086274 AW318849 un08609.y BE371127 601218617 BE22182 601102384 BF719586 mab41h08. BE334491 us796h09.y BE377573 601229761 A1119048 ue93710.y	ACU41109 Sheared D BF167006 601774147. W82115 me98c09.rl BF14026 601788162 BG174120 602334108 BF788835 602110545 AK014354 Mus muscu	GSS 31-MAR-2001 17 end of clone 22E24 of 18 of Anopheles gambiae (African sequence. 18 sequence. 19 acheata; Hexapoda; Insecta; 10 Diptera; Nematocera;
SUMMARIES Query Match Length DB ID	21 21 22 22 15	409 15 473 17 1100 436 22 650 14 166 11 222 14 393 23 494 24	0000000000	4.9 479 8 AA497438 4.9 483 165 BE290613 4.9 546 258 TA193A020 4.9 547 143 BF01664 4.9 552 166 B8303625 4.9 553 114 AW318849 4.9 550 165 BE282182 4.9 590 165 BE282182 4.9 590 165 BE28218491 4.9 692 166 BE334491 4.9 692 166 BE37573	755 760 760 760 760 760 760 760 760	CNSOIMQH 830 bp DNA Anopheles gambiae BAC end sequence T7 end Notrebamel library from strain PEST of An malaria mosquito), genomic survey sequence AL151258 GI:7011737 GSS. AL51258.1 GI:7011737 GSS. Anopheles gambiae Eukaryota; Metazoa; Arthropoda; Tracheata Pterygota; Neoptera; Endopterygota; Dipte Culicoidea; Anopheles. 1 (bases 1 to 830) Genoscope.

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RESULT 1 CNSO1MQH LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

/organism="Homo sapiens"

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d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 2084)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                587 ATATMCCGYGAWWTDWAAAATTTTACMTCAWACAATATACGATGTGCAKTGANTCTTAYT
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/plasmid="BeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN14D20"
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TITLE
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COMMENT
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source

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/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI size susing the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (stratagene) and Superscript IRT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostel; Euteleostei; Neoteleostei; Acanthooropha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 911)

Rost-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Welssenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   911 bp DNA GSS 15-MAY-2000 nigroviridis genome survey sequence T7 end of clone library G from Tetraodon nigroviridis, genomic survey
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                                                                 /tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   59;
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 37.2; DI
Pred. No. 2.1;
0; Mismatches
                  /clone="IMAGE:4053392"
/clone_lib="NIH_MGC_46"
/db_xref="taxon:9606
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                           Library."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="204B10"
/clone="11b="G"
/note="Genoscope sequence ID : C0AG204DA05Lp1-end : T7"
/note="Genoscope sequence ID : C0AG204DA05Lp1-end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="retina"
/lab_host="retina"
/lab_host="DH10B (phage-resistant)"
/note="lorgan: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full:length clones and constructed by Life Technologies.
In a NH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG342366 1018 bp mRNA EST 27-FEB-2001
602374287F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4481877 5',
BG342366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                              ggtaagcgatgccaccccagcgcataatatcgagcacgatcggcgcggcattggacaaaa 160
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:4481877"
/clone_lib="NIH_MGC_94"
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ub14c04.rl Stratagene mouse macrophage (#937306) Mus musculus cDNA clone IMAGE:1366950 5' similar to SW:PRSX_HOWAN Q92524 26S PROTEASE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousesest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
                                                                                                                                                                                                                                             191 AAGTAGCATTCCCCTTTTAAATGTTGGTGTAACATCTTTGTTTTTTATGAAACCAGCTTGA 250
                                                                                                                                                                                                                                                                                                                      348 gacctatggaagtacttaagtaatgattggttcttaacatggtttaatatgcttcat 407
                                                                                                                                                                                                                                                                                                                                                                              311 GAGATATCTGCCAAGAGAGGTGGATCCATTGGTTTATAAAACATGTCTCACGAGGATCCTG 370
                                                                                                       228 aatgagteettegegettaatteettgtttaateaeeagtaeattetgeggteegatgga 287
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                                                     Indels
Score 37; DB 152; 1
Pred. No. 2;
0; Mismatches 105;
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/db_xref="taxon:10090"
/clone="IMAGE:1366950"
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The WashU-HHMI Mouse EST Project
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5.2%;
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Matches 100; Conservative
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Web: www.genoscope.coms.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk ... This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etded un Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                       CNSO14RI 1100 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN12G24 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
                                                                                                                                                      278 giccgaiggacagiaaaagaciggcccccaaaagcagaccigiaaigaagaiiiccaiga 337
                                                                                                                                                                                                 220 GTCAGCTTGACAAAAGTAAGCTGAAGCCAGGAACCAGAGTTGTTTGGATATGACCACAC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 ggtaagcgatgccaccccagcgcataatatcgagcacgatcggcggcgtcgttggacaaaa 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                            338 tcaccatcgtgacctatggaagtacttaagtaaaatgattggttcttaacatggttta 395
                                                                                                                                                                                                                                                                   1055 GGGVRGMAVGGVGVWMMRGGGGGMMMGGGGGMMRGVRGVRGMAGGGGGMAGAGRAKGAGAGARR
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                                                                 DB 17;
                                                               Score 36.4; DB Pred. No. 2.5; 0; Mismatches
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11.7%; Pred. No. 3.6;
Live 118; Mismatches
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Plasmid Drosophila melanogaster
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/db_xref="taxon:7227"
/clone_lib="brosBAC"
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1. .1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="BACN12G24"
/note="end : SP6"
175 c 118 g
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                                                                 5.1%;
                                                                                                             67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 473)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Organ: mammary gland; Vector: pT713D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco PI; 1st; 1st strand cDNA was primed with a Not I · oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                   278 gtccgatggacagtaaaagactggcccccaaaagcagacctgtaatgaagatttccatga 337
                                                                                                               Gaps
                                                                                                                                                                                 A1174155 473 bp mRNA EST 07-0CT-1998 vz84d11.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1333173 5' similar to SW:PRSX_HUMAN Q92524 26S PROTEASE REGULATORY SUBUNIT P42. ;, mRNA sequence.
                                                                                                                                                                                                                                          338 tcaccatcgtgacctatggaagtacttaagtaaaaatgattggttcttaacatggttta 395
                                                                                                                                                                                                                                                                   .
0
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Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                 Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 FT from Amersham High quality sequence stop: 451.

Location/Qualifiers
                                                                                                          Indels
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/sex="male"
                                                                                                          51;
                                                                 DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="mammary gland"
/dev_stage="4 weeks"
                                                               Score 36.4; D
Pred. No. 2.4;
                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:1333173"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI174155.1 GI:3720297
                                                               5.1%;
                                                                                    Best Local Similarity 56.8
Matches 67; Conservative
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Fax: 314 286 1810
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Length 436;

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Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Petrygota; Meoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[ Dases 1 to 650]

1 (Dases 1 to 650]

2 (Calson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J.,

Park, S., Paragas, V., Phousenavong, S., Wan, K., Yu, C., Lewis, S. E.,

Celniker, S. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="AT Drosophila melanogaster adult testes pOTB7"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_grage="0-3 day old Ore-R males"
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/note="Organ: ADULT testes; Vector: pormB7; Site_1: ECORI;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pormB7. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF485823 650 bp mRNA EST 16-APR-2001
AT1987.5 prime AT Drosophila melanogaster adult testes poTB7
Drosophila melanogaster cDNA clone AT18875 5 similar to CG13768:
FBan0013768 last_updated:000321, mRNA sequence.
                                                                                                                                                                                       tggtgttgctgcaagcagaaactaaagcgcaactatctggacgccttgctgaaatcccgt 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AR003614
Plate: AT.198 row: G column: 3
High quality sequence stop: 633.
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/db_xref="taxon:7227"
/clone="AT19875"
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                                                                        37;
5.1%; Score 36; DB 228; 60.6%; Pred. No. 3.2;
                                                                                                                                                                                                                                                                                          674 taaccatcgccatcaacgcagattcgctatccac 707
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0; Mismatches
                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                127 TCCCCATCCCCATCTTCCTCCATCNCATCCC 94
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1. .650
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Matches 52; Conserv
                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High Throughbut Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Tex: (206) 616-3887 Tel: (206) 616-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holzman, T.,
Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A0405681 436 bp DNA GSS 13-MAR-1999 HS_5076_A1_A11_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=652 Col=21 Row=A, DNA sequence.
NNNWAKMNNNNKTNNNANNKNNNMANNNKNNNKNANNNKNTNNKTMMMNNKNNNN 756
                                                                                                                                                                                                                                                399 tagetteatgaaceceatteaactggacaetttgeteteaateattgatgaaggeagett 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695 GNGNNNNNAGNMMANNGNNNNANGTTNTGNNCGCMGNNGNCNNTNNNNNGNNNNTTGN 636
                                                                                                          caccatcgtgacctatggaagtacttaagtaaaatgattggttcttaacatggtttaata
                                                                                                                                                                                                                                                                                                                         755 NMKCNMMNNNNMMMNNTKNMNNMMNNTNNNTNNNTTNMNNMMNTNMNNMTNMNNNN
                                                                                                                                                                                                                                                                                                                                                                                             cgaaggcgcctccttagccctttccatttcccctcggcggtgagtcagcgcgttaaagc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 436)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="Hexon:9606"
/clone="Plate=652 Col=21 Row=A"
/clone_lib="RPCI-11 Human Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 436.
Location/Qualifiers
1. 436
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Seg primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       635 MNNNNNMMANAAAAGNNGANAAG 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĀQ405681
AQ405681.1 GI:4415669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           519 tctcgagcatcacgtgggtcgag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS

JOURNAL MEDLINE COMMENT

TITLE

RESULT 9 AQ405681/c DEFINITION

459

339 815

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421 ctggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagccctt 480
                                                                     Gaps
                           0;
Length 650;
                           27; Indels
Score 35.8; DB 149;
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Source

FEATURES

BASE COUNT ORIGIN

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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

RESULT 11 AW351850/c

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DEFINITION

LOCUS

ACCESSION

VERSION

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Cidone_lib="HP0619"

/dev_stage="Adult"
/dev_stage=
                              Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 222)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Solai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carralho,A.F., Matsukuma,A., Waia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ851405 393 bp DNA GSS 13-APR-2001 LMAJFV1_lm40b11.yl Leishmania major FV1 random genomic library Leishmania major genomic clone LMAJFV1_lm40b11 5', DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 222
/organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence start: 60
High quality sequence stop: 91.
Location/Qualifiers
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Leishmania major
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SOURCE
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ORIGIN
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AQ851405
                                                                                                                                            REFERENCE
AUTHORS
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
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/organism="Homo saplens"
/db.xef="texaon:9606"
/clone_lib="CT0199"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: +55-11-2704092

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-CT0199-

180999-012-A094c3=1999-09-18&t4=1)
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                                                                                                                                                                                                                                                                                                                                AW351850 166 bp mRNA EST 01-FEB-2000 RC1-CT0199-180999-012-A09 CT0199 Homo sapiens cDNA, mRNA sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 tttcgctgccatgacggcaaaccataacaggtaagcgatgccaccc 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 GGATCCCGGCCTGTCGACTTCCCGCACGATGTGAGTTATGCCAGCC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35.6; DB 115;
Pred. No. 3.3;
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High quality sequence stop: 166.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                               AW351850
AW351850.1 GI:6849563
                                                       248 TCCACCGACACCTTGGCAG 266
481 tecattteeceteggegg 499
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1 Similarity 58.5%;
62; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 166)
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FEATURES

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Gaps

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Leishmania. 1 (basea 1 to 393) Akopyants, N.S., Clifton, S.W., Martin, J., Pape, D., Wylie, T., Li, L.,

REFERENCE AUTHORS

nemur EST

ACCESSION VERSION KEYWORDS' SOURCE

LOCUS

RESULT 12

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BF352878

Query Match

Matches

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BASE COUNT ORIGIN

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

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/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
/cultivar="B73"
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Other_GSSs: RPCI-23-94A11.TJ
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AZ253065.1 GI:8566268
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ilarity 51.9%;
Conservative
                                                                            1 (bases 1 to 492)
Walbot, V.
                                                                                                                                             University
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                      .492
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/strain="Friedlin strain VI"
/db_xref="taxon:564"
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/clone="hwhytr1"_im40bl!"
/clone=lib="refishmania major FVI random genomic library"
/lab_host="Top10 (Invitrogen)"
/lab_host="Top10 (Invitrogen)"
/note="weetor: pZero-2 (Invitrogen); Site_1: EccRV;
Genomic DNA was isolated from stationary phase cells. For this library, DNA was sheared to give a tight size distribution of 1-1.5kb fragments, blunt-ended with T4 DNA polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into pZero-2 vector's EccRV site."
55 a 97 c 116 g 75 t
Kissinger, J., Roos, D.S., Marra, M., Hillier, L., Chinwalla, A., Blistain, A., Schmitt, A., Person, B., Theising, B., Ritter, E., Ronko, J., Bennett, J., Coller, R., Underwood, K., Cardenas, M., Gibboons, M., Harvey, N., McCann, R., Tsaqareishvili, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R., Wilson, R. and Beverley, S.M. A survey of the Leishmania major Friedlin strain V1 genome by shotgun sequencing: a resource for DNA
Mol. Biochem. Parasitol. 113 (2), 337-340 (2001)
Cother, GSSs: Imd0bl. X.
Contact: Akopyants, NS / Beverley, SM
WashU Leishmania project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
Library construction: Natalia S. Akopyants, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain VI genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
clone material please contact: Natalia S. Akopyants Ph.D.
(natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.
(Seq primer: -40RP from Gibco
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683016G08.x1 683 - 14 day immature embryo from Hake lab (HS) Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     564 ggccaaagcaaccgaagcgggtgaagtccttgtgcaagcagcgcggaaaatggtgttgct 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 GTCCGTAGCGGCAGTGCTGCGAGAACCTCACCCTCAAGCAGCGCGAGTTGCTGGTGCGGGCT 244
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Matches 74; Conservative
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ORGANISM

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/clone_lib="683 - 14 day immature embryo from Hake lab (HS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ253065 494 bp DNA GSS 15-JUN-2000
RPCI-23-94A11.TV RPCI-23 Mus musculus genomic clone RPCI-23-94A11,
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; 2ea.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 494)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Express); Site_1: XhOI; Site_2: EcoRI; Directionally cloned, 14 day immature embryo library created with Stratagene's Zap Express cDNA protocol."

97 c 154 g 116 t
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                                                                                                                                                               Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                                                        Contact: Walbot V
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
Fax: 650 725 8227
Fax: 650 725 8227
Fax: 683016 row: G column: 08
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="embryo"
/dev_stage="14 days after pollination"
/lab_host="DH10B"
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Pred. No. 4.4;
0; Mismatches
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Department of Eukaryotic Genomics
The Institute for Genomic Research
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
CooRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

71 c 73 g 130 t
                                                                          Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieterédejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: T7
Class: BAC ends.
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="RPCI-23-94A11"
/clone_lib="RPCI-23"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
                               Tel: 301 838 0200
Fax: 301 838 0208
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ô 241 cgcttaattccttgtttaatcaccagtacattctgcggtccgatggacagtaaaagactg 300 0; Gaps Score 35.6; DB 240; Length 494; Pred. No. 4.4; 0; Mismatches 84; Indels 0; 5.0%; Query Match Best Local Similarity 50.6 Matches 86; Conservative ò

318 CTCTAAAACATTTTTTTAAAAAAGTCTATTTCCCCAAATGAAGATGATAAATCCACCT 377

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301 gcccccaaaagcagacctgtaatgaagatttccatgatcaccatcgtgacctatggaagt 360 g à

378 AATCCTATAACAAAAGACCCAACAATGATTACCATGCTTGACATAATGAATAGTCAAAT 437

361 acttaagtaaaatgattggttcttaacatggtttaatatagcttcatgaa 410 ö

Search completed: September 14, 2001, 06:59:12 Job time: 12059 sec

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Oligonucleotide D2
Oligonucleotide D1
Sequence of BamHI/
P. aeruginosa tfdA
N. meningitidis pa
Neisseria meningit
Gene encoding a su
Oligonucleotide D1
Oligonucleotide D2
Oligonucleotide D4
Human Secreted D2
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N. meningitidis pa
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/*tag= c
/label= orf3
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AAA10594
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AAF5826259
AAF58262
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AAA39105
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AAA93617
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/label= LysG
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                     LySE and ORR3 genes. LysG and LySE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-cerrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.

NB. This sequence has been created from the information given in table 2
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  (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
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Corynebacterium glutamicum MP protein nucleotide sequence SEQ ID NO:53.
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                     gcagcgcggaaaatggtgttgctgcaagcagaaactaaagcgcaactatctggacgcctt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200100843-A2
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99DE-1033006 99US-0148613

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Corynebacterium glutamicum MP protein nucleotide sequence SEQ ID NO:49
                                                                                                                                                                                                                                            fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
                        16
                                                                                                                                                                                                                                Corynebacterium glutamicum; metabolic pathway protein; MP protein;
BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                          990E-1031415.
99DE-1031418.
99DE-1031420.
99DE-1031424.
99DE-1031424.
99DE-1031434.
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99DE-1031453.
99DE-1031457.
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99DE-1031478.
99DE-1031510.
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99DE-1031592.
99DE-1031632.
                                                                                                                                   AAF71777 standard; DNA; 993
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99DE-1032126
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99DE-1040764
                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum.
                                                                                                                                                                                   (first entry)
                                                ctggacactttgctc 435
                                                             CIGGACACITIGCIC 1
                                                                                                                                                                                                                                                                                                                                WO200100843-A2.
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08-JUL-1999;
08-JUL-1999;
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08-JUL-1999;
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08-JUL-1999;
08-JUL-1999;
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08-JUL-1999;
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                                                                                                                                                          AAF71777;
                                                421
                                                                        15
                                                                                                                       AAF71777
                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyraimidine bases, nucleosides, nucleotides, incloding bases, nucleosides, nucleotides, carbonydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
                                                                                                                                                                                                                                                                                                                                           pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gococcaaaagcagacctgtaatgaagatttccatgatcaccatcgtgacctatggaagt 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids from Corynebacterium glutamicum encoding metabolic
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Ö
                                                                                                                                                                                                                                                                       Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.2%; Score 435; DB 22; Length 822; 100.0%; Pred. No. 8e-133; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 822 BP; 167 A; 192 C; 246 G; 217 T; 0 other;
                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                       Zelder
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                                                                                                                                                                                                                                                                       Schroeder
                                   99DE-1040832.
99DE-1041378.
99DE-1041379.
                                                                      99DE-1041380.
99DE-1041394.
99DE-1041396.
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99DE-1042077.
99DE-1042086.
99DE-1042088.
99DE-1042088.
                        99DE-1040766
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99DE-1042129
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Best Local Similarity 100.
Matches 435; Conservative
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                                                                                                                                                                                                                                                                      Pompejus M, Kroeger
                                                                                                                                                                                                                                                                                             WPI; 2001-137957/14.
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                                                                                                                                                                                                                                              (BADI ) BASF AG.
                        27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
                                                          31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
                                                                                                                                03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
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03-SEP-1999;
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attenuation; gene deletion;

BP.

/*tag= a /note= "BCG delta 1 deletion region"

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Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect bacterial infection
delta 2; virulence; avirulence; attenuati
obacteria; vaccine; infection; marker; ss
                                                                                                                               BCG deletion region 2 and flanking sequences
                                                                                                                                                                                                        Location/Qualifiers
3382..14071
/*tag= a
                                                                                                                                                                                    bovis strain BCG
                                                              AAT33536 standard; DNA; 15239
                                                                                                                                                                                                                                                                                                         96WO-US01938
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                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                   (PATH-) PATHOGENESIS CORP.
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                                                                                                                                                                 mycobacteria;
                                                                                                                                                                                     Mycobacterium
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misc_feature
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                                                                                     AAT33536;
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                                                                                                                                                    BCG
                                                     AAT33536
           qq
                                                                         8XCCCCCCCCCCCCCX8X4414X8X5X5X5X5X5X544444X8X6X6X
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                                                                                                                                                                                                                                                                                  Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purline and pyrimidine bases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttcccctcggcggtgagtcagcgcttaaagctctcgagcatcacgtgggtcgagtgtt
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                                                                                                                                                                                                                               Haberhauer G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 406; DB 22; L
Pred. No. 3.1e-123;
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0
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100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 226-228; 1737pp; English.
                                                   99DE-1041380.
99DE-1041394.
99DE-1041396.
                              99DE-1041378
99DE-1041379
                                                                                  99DE-1042076
99DE-1042077
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99DE-1042086
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99DE-1042088
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Best Local Similarity 100.
Matches 406; Conservative
                                                                                                                                                                                                                              Kroeger B,
                                                                                                                                                                                                                                                 WPI; 2001-137957/14.
P-PSDB; AAB79658.
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                                                                                                                                                                                                          (BADI ) BASF
                                                                                                                                                                                    09-MAR-2000;
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                              31-AUG-1999,
31-AUG-1999,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctttccatttcccctcggcggtgagtcagcgttaaagctctcgagcatcacgtgggt 537
                                                                         This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdelta2. A specific genetic deletion of this region results in an avirulence phenotype of the mycobacterium. 2 Other deletion regions (see AAT33535 and AAT33537) have also been detected. Identification involved screening a BCG cosmid library with a radiolabeled probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H37Rv and avirulent BCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the deletion; the deletions are detected either by detecting the presence or absence of deletion junctions (see AAT3518 46), or by detecting the presence or absence of the sequences contained within the deletion. Deletion polypeptides are used as components of
                                                                                                                                                                                                                                                                                                                                                                The deletions provide useful markers for the identification of an avirulent, or a virulent, mycobacterial phenotype. Determination of avirulence requires the detection of the presence or absence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 17; Length 15239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.9%; Score 63.2; DB 17;
55.3%; Pred. No. 7.4e-10;
iive 0; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunological assays and in vaccines
Example 1; Fig 2; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 166; Conserv
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51

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Genomic library; bacteria; human upper airway; otitis media; sinusitis;
                                                                                                                    atgagiceticgogetiaaticetigitiaateaceagiacaticigeggieegaiggae 288
tecacettgtttgtcatggcgtcttcgctgccatgacggcaaaccataacaggtaagcg 108
                                                                                        atgccaccccagcgcataatatcgagcacgatcggcgcggcattggacaaaagatcaacg 168
                                                                                                                                                                                                                           170 CCAAAAATCCCGGCGAAATCAGGACCAAATCGCTGATAGCACAAAGTAAGGCAATCATA 111
                            289 agtaaaagactggccccaaaagcagacctgtaatgaa 326
                                                                                                                                                                                                                                                                                                                                                                                          bronchopulmonary; endocarditis; meningitis; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-2000; 2000WO-US16649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lagace RE, Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-1999;
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  49
                                                                                        109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the yggA gene (an excretion protein gene) of Escherichia coli. The amino acid excretion protein produced from this gene is involved in the production of amino acids, and an increase in its expression leads to an increase accumulation of amino acids in the cell. In this case, an increase in arginine, glutamic acid and lysine is achieved if multiple copies of the gene are transfected into a bacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production of L-amino acids by an Escherichia bacterium increasing the expression amount of an L-amino acid excretion
5313 ctacatgtcacccctcggctgtcagtcagcgcatcaagtcgttggagcagcagtcggc 5372
                                                                                        caggtgctggtggtcagggaaaagccatgtcgggcgacgaccgcaggtatcccgctgttg 5432
                                                                                                                                                             gccttgctgaa----atcccgttaaccatcgccatcaacgcagattcgctatccacatgg 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakanishi K, Aleshin VV, Troshin PV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E. coli; yggA gene; amino acid production; excretion protein gene; amino acid excretion protein; ds.
                                             cgagtgttggtatcgcgcacccaaccggccaaagcaaccgaagcgggtgaagtccttgtg
                                                                                                                                     caagcagcgcggaaaatggtgttgctgcaagcagaaactaaagcgcaactatctgg--ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 24; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "YggA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The bacterium used is E. coli.
                                                                                                                                                                                                                                                                                                                                                           AAA52691/c
ID AAA52691 standard; DNA; 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zakataeva NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99EP-0125263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98RU-0124016.
99RU-0104431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli yggA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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P-PSDB; AAB01789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Livshits VA,
Tokhmakova IL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1016710-A2
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09-MAR-1999;
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protein -
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The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF28554, The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as olitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                  Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 45613;
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Pred. No. 0.00098;
                                                                                                                                                                                                                                                                                                          Claim 1; Page 180-191; 545pp; English.
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WPI; 2001-041427/05
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Best Local Similarity
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Gaps

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Length 636; Indels

Score 60.4; DB 21; Pred. No. 1e-09; 0; Mismatches 136;

8.58;

Query Match
Best Local Similarity 51.13
Matches 142; Conservative

ΚĽ; Berg 1461 CACTCTTGCTGCTGTTGCTGACGCAGGATCTCTCGACGGTGCAGCGCATGAACTCCGCAT 1402

ttocccctcggcggtgagtcagcgcttaaagctctcgagcatcacgtgggtcgagtgtt 1401 TACTCCCTCCGCTGTGAGCCAGCGGCTCAAGGCTTTGGAGACTCTTCTTGGTCAGGTCGT 546 ggtatcgcgcacccaaccggccaaagcaaccgaagcgggtgaagtccttgtgcaagcagc

486

1341 ATTGGTGCGCTCAAAGCCAGTGCGTCTGACGAGCACCGGGGGCGTCCATCGTTCGGTTTGC 1282

606 geggaaaatggtgttgetgeaageagaaae

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a Stealth virus nucleic acid clone. The invention relates to a method of detecting and characterising a stealth virus by reacting a sample suspected of containing a stealth virus with a probe from a known stealth virus and sequencing the resultant isolated nucleotide. The method comprises the steps of: (a) isolating DNA or RNA from a sample suspected of containing a stealth virus, e.g. a culture of cells showing a viral cytopathic effect; (b) testing the reactivity of the isolated DNA or RNA with a molecular probe that contains at least 18 identified from a stealth virus; and, optionally (c) sequencing the isolated DNA or RNA molecules that react with the probe. The method is used to detect stealth virus in a biological product, food or in the
                                                                    inhibitory or stimulatory effects on stealth virus replication and to determine capacity of the virus to recombine with and potentially alter the nucleic acid sequences of a cell or bacterium.
                                             10609 ATGAATACCACAAATCTTGCCACTTTTGTTGCAGTTATGCAGACAGGCAGCATCTCTAGT 10550
                      406 atgaaccccattcaactggacactttgctctcaatcattgatgaaggcagcttcgaaggc 465
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           environment. The method is also used to evaluate agents for their
 0;
 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4915 BP; 967 A; 1521 C; 1591 G; 828 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45.2; DB 20;
Pred. No. 0.00032;
0; Mismatches 103;
                                                                                                                                                                                                                                                                                                   Stealth virus; detection; diagnosis; infection;
                                                                                                                                                                                                                                                                             Stealth virus nucleic acid clone, SEQ ID NO: 9.
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 19; Page 40-42; 95pp; English.
                                                                                                                                            10489 GATGAATTTGGGACGGCGTTGTT 10467
                                                                                                                     catcacgtgggtcgagtgttggt 548
                                                                                                                                                                                                      AAX84317 standard; DNA; 4915 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel strains of stealth virus
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Best Local Similarity 51.0%;
Matches 107; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0001184
                                                                                                                                                                                                                                                     (first entry)
 Conservative
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                                                                                                                                                                                                                                                                                                                          Stealth virus
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82;
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AAX84317/C
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group, useful as labels in allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 ttaattccttgtttaatcaccagtacattctgcggtccgatggacagtaaaagactggcc 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 atgaacaaaaagacgtcagaaattaaacacacgagaagaaccgcaatgagtccttcgcgc 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 936;
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                                                                                                                                                                                                                                                                                                                             Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
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53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping,
1281 TCGTCAGACCGAGATGCTCGAGAGGGAGAC 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CLIN-) CLINICAL MICRO SENSORS INC.
                                                                                                                           AAF58252 standard; DNA; 936 BP
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                                           Oligonucleotide D1835
                                                                                                                                                                                                                                                                                                                                                       gene expression; ss
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Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                       AAF58252;
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                       364 taagtaaaatgattggttcttaacatggtttaatatagcttcatgaaccccattcaactg 423
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                                                                                              424 gacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagccctttcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Page 127; 159pp; English.
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Best Local S
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                                                                                                                                                                                                             The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
  cccaaaagcagacctgtaatgaagatttccatgatcaccatcgtgacctatggaagtact 363
                                             taagtaaaaatgattggttcttaacatggtttaatagcttcatgaaccccattcaactg 423
                                                                                                                      WANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNERWANNER
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5.8%; Pred. No. 0.034;
11ve 163; Mismatches 130;
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17-MAR-2000; 2000US-0190259.
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Best Local Similarity
Matches 18; Conserv
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17-MAR-2000; 2000US-0190259
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17-MAR-2000; 2000US-0190259
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812 cccccccc 822
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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WPI; 2001-159728/16.
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                                                                                                       244 ttaatteettgtttaateaecagtaeattetgeggteegatggaeagtaaaagaetggee 303
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                                                                                                                                                                                                                                                                                  Sequence of BamHI/Sall fragment of the tfdA gene which encodes 2,4-dichlorophenoxyacetic acid (2,4-D) mono-oxygenase.
                                                                    The tfdA gene product is a 2,4-D decomposing protein. A.eutrophus JMP 134 contains an 80 kb plasmid, pJP4, which carries the genes coding for 2,4-D decomposition. Plasmids and bacteria contg. the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmids and bacteria contg. gene tfdA for 2, 4\text{-}D\text{-}mono\text{:}oxygenase} isolated using new Alcaligenes eutrophus transposon mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herbicide resistance; halogenated aromatic cpd; enzyme;
18; Conservative 163; Mismatches 130;
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/note= "DNA SQ claimed"
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748..1608
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(STRE/) STREBER W.R.
(MACQ-) MACQUARIE UNIV.
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 atgaacaaaaagacgtcagaaattaaacacacgagaagaagcaccgcaatgagtccttcgcgc 243
                                                                    ttaattccttgtttaatcaccagtacattctgcggtccgatggacagtaaaagactggcc 303
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                                 Length 938;
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17-MAR-2000; 2000US-0190259.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF58255;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
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184
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AAF58255

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gene are useful for prodn. of 2,4-D mono-oxygenase and for transferring the ability to decompose 2,4-D to other micro-organisms (which could then be useful for cleaning waste water polluted by halogenated aromatic cpds.) or to plants (to impart tolerance to 2,4-
                                                                                                                                                                                                 418 caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc 477
                                                                                                                                                                                                                   478 ctttccatttccccctcggcggtgagtcagcgcgttaaagctctcgagcatcacgtgggt 537
                                                                                                                                                                                                                                                                               Using presence of tfdA gene to select transgenic plants - imparting resistance to 2,4-di:chloro:phenoxy:acetic acid, esp. sweetgum (Liquidamber) trees contg. this gene and plantations of them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic plant; tfdA gene; 2,4-dichlorophenoxyacetic acid; 2,4-D; herbicide resistance; sweetgum; Liquidamber styraciflua; hardwood; plantation; crop improvement; selectable marker; pUCW200; vector;
                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A tidA gene of P. aeruginosa plasmid pR0101, which encodes the enzymes for 2,4-D degradation, was cloned into Agrobacterium tumefaciens vector pB1121 to form pUGW300. This was used to introduce 2,4-D herbicide-resistance into sweetgum, thereby
                                                                                                                                     Score 37; DB 9; Length 2058;
Pred. No. 0.098;
0; Mismatches 65; Indels
                                                                                          Sequence 2058 BP; 372 A; 659 C; 661 G; 366 T; 0 other;
                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
751..1611
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig.7; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            AA097857 standard; DNA; 2058 BP
                                                                                                                                                                                                                                                                                                                     538 cgagtgttggtatcgcgcacc 558
                                                                                                                                                                                                                                                                                                                                                     410 GTGTTGTTCGAGCGCAGC 390
                                                                                                                                      Query Match 5.2%;
Best Local Similarity 53.9%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US00284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0358117
94US-0179667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-DEC-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P. aeruginosa tfdA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UNBC ) UNION CAMP CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.
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P-PSDB; AAR79659.
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418 caactggacactttgctctcaatcattgatgaaggcagcttcgaaggcgcctccttagcc 477
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                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                530 CAGCITCGCIATITCGTTGCTGCCGCGGAGGGCCAACGTCGGTGCCGCCGCGCGGGG
allowing selection of transgenic plants and reducing the cost of site prepn. and maintenance.
                                                                                                                                        .;
0
                                                                                                      Score 37; DB 16; Length 2058; Pred. No. 0.098;
                                                   Sequence 2058 BP; 372 A; 659 C; 661 G; 366 T; 0 other;
                                                                                                                                        65;
                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: September 14, 2001, 07:54:24 Job time: 8873 sec
                                                                                                                                                                                                                                                                                                                                         410 GTGTTGTTGTTCGAGCGCAGC 390
                                                                                                                                                                                                                                                                                                                   538 cgagtgttggtatcgcgcacc 558
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Best Local Similarity 53.99
Matches 76; Conservative
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Table 1	
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								RE	O X	X Y	TO X	X DE	KW	XX SO
	Seconds updates/sec	N 216			,						- 12 - 12 - 12 - 13			
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	<pre>protein search, using sw mode! September 13, 2001, 17:33:09 ; Search time 34.57 Se (without alignments) 378.790 Million cell u</pre>	US-09-105-1171-2 11 091 1 DIPLEETMYALRDIVASGKASHDAGINIWAKATDSKTREN 1: BLOSUM62		of hits satisfying chosen parameters: 412676	<pre>seq length: 0 seq length: 2000000000</pre>	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	A_Geneseq_0601:* 1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:* 2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:* 3: SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:* 4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:* 5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:* 6: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:* 7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:* 8: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:* 8: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*		` ' '	` ` `	` ' '	18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:* 19: /SIDS8/qcgdata/qeneseq/geneseqp/AA1998.DAT:*	. ' '	22: /SIDSB/gcgdata/geneseqf/geneseqp/AA2001.DAT:*
	OM protein - Run on:	Title: Perfect score: Sequence: Scoring table:	Searched:	Total number of	Minimum DB s Maximum DB s	Post-process	Database :							

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	C. glutamicum orf3	Corynebacterium gl 🖈	Escherichia coli p.	Shaker-like potass	Shaker-like potass	Zea mays protein f	Zea mays protein f	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	
	ID	AAW37716	AAB76844	AAY52837	AAW23388	AAW23389	AAG35920	AAG35919	AAG09266	AAG39051	AAG39050	AAG39049	
	DB	18	22	20	18	18	21	21	21	21	21	21	
	Ouery Match Length DB ID	216	290	348	329	329	266	328	216	216	266	328	
#P	Ouery Match	100.0	72.6	20.6	18.8	18.5	17.9	17.9	17.9	17.9	17.9	17.9	
	Score	1001	792	225	205	202	195.5	195.5	195	195	195	195	
	Result No.	-	7	m	4	S	9	7	œ	6	10	11	

Corynebacterium gl Corynebacterium gl Corynebacterium gl Zea mays protein f Arabidopsis thalia Mouse mCPRMI allel Arabidopsis thalia	rotein; export protein; ditive. especially lysine - nding gene from
22 AAB79618 22 AAB80067 22 AAB80067 21 AAG35251 21 AAG35251 21 AAG35250 21 AAG35249 21 AAG39499 21 AAG39499 21 AAG39499 21 AAG39499 21 AAG39206 21 AAG52068 21 AAG52068 21 AAG52068 21 AAG52068 21 AAG52068 21 AAG52068 21 AAG52068 21 AAG5209 21 AAG38206 22 AAY34937 20 AAY49337 20 AAY369903 20 AAW93088 20 AAW93088 20 AAW93099 20 AAW93099 20 AAW93099 20 AAW93099 21 AAG36393 22 AAG36393	ALIGNMENTS; 216 AA. ransport; regulatory p o acid; animal feed ad cacid; animal feed ad 2. 2. TUELICH GMBH. jc M; ction of amino acids, r activity or correspo t and regulatory genes
184 16.9 312 180.5 16.5 315 180.5 16.5 315 180.5 16.5 316 175 16.0 333 175 16.0 333 166.5 15.3 324 166.5 15.3 324 166.5 15.3 324 167.5 15.0 334 163.5 15.0 337 163.5 15.0 337 163.5 15.0 386 163.5 14.9 331 162.5 14.9 331 163.5 14.7 331 156.5 14.3 338	AW37716 standard; Proteinman S
11111111222222222222222222222222222222	RESULT AAW3771 LD AA XX XX AC AA C AA C AA C AA C AA C AA

99DE-1032212. 99DE-1032227. 99DE-1032228.

99DE-1032229. 99DE-1032230. 99DE-1032927.

99DE-1033005 99DE-1033006 99DE-1040764 99DE-1040765 99DE-1040831 99DE-1040832

99DE-1040766 99DE-1040830

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09-JUL-1999;
09-JUL-1999;
14-JUL-1999;
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09-JUL-1999;
09-JUL-1999;
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                            This sequence is the Orf3 protein product, involved in lysine production. Ly65 and Ly8E encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as pharmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation;
                                                                                                                                                                                                                                                                            61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLNV 120
                                                                                                                                                                                                                                                                                                          NNIDMVRKLNDIAQERGOSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDSL 180
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                        1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum; brevibacterium lactofermentum; MCT;
                                                                                                                                                                                                    0
                                                                                                                                                                               Score 1091; DB 18; Length 216; Pred. No. 1.3e-102;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum MCT protein SEQ ID NO:670.
                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                             181 NNLEFSDAELEAIDEISHDAGINIWAKATDSKTREN 216
                                                                                                                                                                            Query Match 100.0%; Score 1091;
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 216; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome mapping; genetic engineering
        Disclosure; Page 9; 16pp; German.
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99DE-1031478
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99DE-1032180
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99DE-1032190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                216 AA;
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08-JUL-1999
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                                                                                                                                                 Sequence
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AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in ABB76510 to AAB7647. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.

AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLNV 120
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-haq 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 792; DB; Pred. No. 4e-72 0; Mismatches
                                                                                                                                                                                                                                                                                Schroeder H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 1109; 1119pp; English.
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99DE-1040833.
99DE-1041378.
99DE-1041379.
99DE-1041395.
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Best Local Similarity 99.4%;
Matches 156; Conservative
                                                                                                                       99DE-1042078
99DE-1042079
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                                                                                                                                                                                                                                                                                Pompejus M, Kroeger
                                                                                                                                                                                                                                                                                                                              WPI; 2001-071486/08.
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ID AAY5:
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WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ-----GKSL -----eeeremlplcyqegvavipwsplargrltr-----pwgettarlvsdevgknl

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14-APR-1999; 14-APR-1998; 05-AUG-1998; Miyake K, H Takahashi S; W09953071-A1 15-FEB-1999; Escherichia 21-OCT-1999

63; Indels 26; Gaps 20.6%; Score 225; DB 20; Length 348; 31.9%; Pred. No. 1.6e-14; ive 39; Mismatches 63; Indels 20 Conservative Query Match Best Local Similarity Matches 60; Conserv

DTPLEETWYALRDIVASGKALYVGISSYGPELTAEAAEFWAEEGCPLLIH-QPSYSIINR 59

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114 SEGMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQL 173 156 ntpieetlealndvvkagkaryigassmhasqfaqalelqkqhgwaqfvsmqdhynliyr 215 Claim 15; Pages 51-52; 106pp; English. 174 DNSLDSLN 181 317 g ò 셤 ŏ ŏ The present invention describes the preparation of an isoprenoid compound comprising at least 1 DNA e.g. encoding proteins which elevate the efficiency of the synthesis or DNA encoding a farnesyl pyrolinic producing enzyme. The method of preparation of an isoprenoid compound comprises using at least 1 DNA, a vector, cloned cells, their derivative recombinant DNAs or transformed products in a culture system and extracting the isoprenoid accumulated in the medium. The DNA encodes at least 1 of the following: (a) a compound for activating or catalysing the production of 1-deoxy-b-xylulose-5-phosphate from pyruvic acid and glycerylaldehyde-3-phosphate; (b) an enzyme producing farnesyl pyrolinic acid; (c) a protein which elevates the efficiency of synthesis of isoprenoid compounds and comprises a 3 or 4 amino acid sequence optionally with 1 or more of the amino acids being deleted or substituted or an additional amino acid being inserted; (d) a protein which activates or catalyses the production of 2-c-methylo-erythraticol-compounds and compress the production of 2-c-methylo-erythraticol-compound or reaction and is a string end or hybrid activates a target compound or reaction and is a string end or hybrid of the pNA encoded in (a)-(e). Isoprenoid compounds are useful in drugs to preventing cancer and as immunopotentiators), health foods and antifouling coatings. The isoprenoids also inhibit enzymatic reactions on the non-mevalonate pathway and can be used as antibacterials and herbicides. The present invention. Isoprenoid; microorganism; detection; antibacterial; herbicide; heart disease; osteoporosis; haemostasis; cancer; immunopotentiation; health food; antifouling coating; farnesyl pyrolinic acid; pyruvic acid; 1-deoxy-D-xylulose-5-phosphate; glycerylaldehyde-3-phosphate; 2-C-methyl-D-erythreitol-4-phosphate. Preparation of recombinant isoprenoid compounds useful for treatment of heart diseases, osteoporosis and hemostatis, preventing cancer and Kuzuyama T; Seto H, Hashimoto S, Motoyama H, Ozaki A, coli protein sequence SEQ ID NO:4. Claim 1; Page 70-72; 145pp; Japanese. 98JP-0103101. 98JP-0221910. 99JP-0035739. (KYOW) KYOWA HAKKO KOGYO KK 99WO-JP01987 26-JAN-2000 (first entry) WPI; 1999-620434/53. 1 mmunopotentiation 348 AA; Escherichia coli. N-PSDB; AAZ33162 AAY52837; Sequence

Shaker-like potassium ion channel beta-subunit core region Kv beta 1. Polypeptide(s) derived from Shaker-like potassium ion channel alpha and beta subunits - used to alter potassium ion levels in a cell, e.g. for treating neurological disorders, tumours, metabolic disease Shaker-like potassium ion channel; SPC: beta subunit; core region; KV beta 1; N-terminal A and B box; NAB; treatment; cardiac disease; tumour; auto immune disease. (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE AAW23388 standard; protein; 329 AA. 97WO-US02292. 96US-0606143. (first entry) WPI; 1997-435164/40. e.g. for treating ne and cardiac disease WO9731112-A2. 18-FEB-1997; 23-FEB-1996; 02-APR-1998 28-AUG-1997 AAW23388; Mammalia. Li M; AAW23388

This polypeptide sequence Kv beta 1 consists of the core region of a beta-subunit of a Shaker-like potassium ion channel (SPC). This core region can bind to a polypeptide consisting of the N-terminal A and B box (NAB) domain and the NAB-S1 (the first transmembrane spanning domain) linking region of the alpha-subunit of SPC. The polypeptides or the nucleic acid encoding them can be introduced into the cytoplasm of a cell to modulate the flow of potassium ions through a cytoplasmic cell membrane. Potassium ion channels regulate the action potentials, cardiac pacemaking and neurotransmitter release in excitable tissues. In non-excitable tissues they play important roles in hormone secretion, cell proliferation, cell volume regulation and lymphocyte differentiation. Molecules which bind to the alpha or beta-subunit or putative core region of a beta-subunit respectively, and determining whether or not binding occurs. These polypeptides and the encoding whether or not binding occurs. These polypeptides and the encoding whether or not binding occurs. These polypeptides and the encoding chisorders, e.g. neurological disorders, tumours, metabolic diseases, cardiac disease and autoimmune disease.

329 AA; Sequence

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treatment; cardiac disease;
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N-terminal A and B box;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                                                                   116 GMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDN 175
                                                                                                                                                                                                                                 23; Gaps
                                                                                                                                                        2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEA---AEFMAEEGCPLLIHQPSYSIIN 58
                                                                                                                         DB 21; Length 266;
                                                                                                                        Query Match 17.9%; Score 195.5; DB 21; Length Best Local Similarity 30.1%; Pred. No. 1e-11; Matches 65; Conservative 39; Mismatches 89; Indels
                                                                                                                                                                                                                                                       176 SLDSLNNLEFSDAELEAIDEISHDAGINIWAKATDS 211
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99US-0160815.
99US-0160980.
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99US-0160981.
99US-0161405.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                                                                                                                                  17.9%; Score 195.5;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                               990S-0159295.
990S-0159329.
990S-0159330.
990S-0159331.
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99US-0161993.
99US-0162142.
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           99US-0159293
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99US-0159584
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Best Local Similarity
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13-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
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tresqiqenmkavdviplltpivldkieqv
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990S-0157753.
990S-0157865.
990S-0158029.
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                         9908 - 0.155486 - 9908 - 0.155486 - 9908 - 0.156458 - 9908 - 0.156596 - 9908 - 0.156596 - 9908 - 0.156596 - 9908 - 0.156596 - 9908 - 0.156596 - 9908 - 0.159293 - 9908 - 0.159293 - 9908 - 0.159293 - 9908 - 0.159293 - 9908 - 0.159293 - 9908 - 0.159293 - 9908 - 0.159293 - 9908 - 0.159293 - 9908 - 0.159293 - 9908 - 0.160980 - 9908 - 0.160980 - 9908 - 0.160980 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161360 - 9908 - 0.161
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Best Local Si
Matches 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168
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99DE-1031573
99DE-1031592
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                                                                                                               Conservative
                                                                                                    Similarity
                                                         312 AA;
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08-JUL-1999
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                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 to AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a polyketide, or an enzyme. The presence of (I) or SMP proteins (III) encoded by them are used for diagnosing the presence or activity of Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to C. glutamicum, identify and localise C. glutamicum sequences of interest,
fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 1208-1209; 1246pp; English.
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                                                                                                                                                                                                  99DE-1031420.
99DE-1031424.
99DE-1031428.
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99DE-1031413
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                                                                 Corynebacterium glutamicum
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                                                                                     WO200100844-A2
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                                                                                                                                 23-JUN-2000;
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                                                                                                            04-JAN-2001
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in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH).
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                                                                                                                                                                                                                                                                                                                                               59 RWVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSR-ASQGKSLS-EG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 MLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TPLEETMYALRDIVASGKALYVGISSYGP---ELTAEAAEFMAEEGCPLLIHQPSYSIIN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum MP protein sequence SEQ ID NO:868.
                                                                                                                                                                                                          Length 312;
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                             16.9%; Score 184; DB 22; 29.9%; Pred. No. 1.9e-10; tive 34; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 LDSLNNLEFSDAELEAIDEIS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 lka-esvtlptpitqalddvs 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99DE-1031415.
99DE-1031418.
99DE-1031419.
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99DE-1031428
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99DE-1031478
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99DE-1031541
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membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation;
117 MLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNS 176
                                                          ||: ::|| : ||| :
                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum; brevibacterium lactofermentum; MCT;
                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum MCT protein SEQ ID NO:672.
                                                                      238 yldnrgriivdaldtaakglgispavtattwvrdrpg
                                                                                                                                                                                                                                                                                                                                                                              genome mapping; genetic engineering
                                                                                                                                                                                                    AAB76845 standard; Protein; 315 AA.
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| lka-esvtlptpitqalddvs 311
                                                                                                    LDSLNNLEFSDAELEAIDEIS 197
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99DE-1031563.
99DE-1032122.
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99DE-1032190
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99DE-1032227
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99DE-1040764
                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum
                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200100805-A2.
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                                                                                                                                                                                                                                AAB76845;
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               184
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                                                                                                                                                                                       AAB76845
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                                                                                                                                                                                                      δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microcyanisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89; Indels 18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.9%; Score 184; DB 22;
29.9%; Pred. No. 1.9e-10;
tive 34; Mismatches 89;
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99DE-1032228.
99DE-1032229.
99DE-1032230.
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99DE-1040766.
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99DE-1041379.
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99DE-1032926
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99DE-1033005
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99DE-1042079
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99DE-1042087
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Best Local Similarity
Matches 60; Conserv
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31-AUG-1999;
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(BADI) BASF AG.

RWVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSR-ASQGKSLS-EG 116

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99US-0137724.
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99US-0132863
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99US-0134219
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99US-0139452
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99US-0144005
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
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                                                                                                                                                                                                                                                            AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum or related bacteria, as reference points for mapping C. glutamicum, and as markers for transformation.

AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention.
                                                                                                                     Corynebacterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 PGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYL--DGIPEGSRASQ-GKSLSEGMLNV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWVEE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 -kdyeenvqplaekhgvavfpyfalaaglltgkytskedisgkaragqldryasdeafav
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                     Haberhauer G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.5%; Score 180.5; DB 22; Length 315; 29.4%; Pred. No. 4.4e-10;
                     Zelder O,
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                                                                                                                                                                                                                       Claim 20; Page 1111-1112; 1119pp; English.
                     Schroeder H,
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99US-0123548.
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Best Local Similarity 29.44
Matches 58; Conservative
                     Pompejus M, Kroeger B,
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                                                         WPI; 2001-071486/08.
N-PSDB; AAF68078.
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05-MAR-1999;
09-MAR-1999;
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990S-01443313.
990S-0144333.
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990S-0144333.
990S-0144335.
990S-0145086.
990S-0147302.
990S-01463319.
990S-01463319.
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990S-01463319.
990S-0146339.
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30-A0G-1999;
31-A0G-1999;
31-A0G-1999;
31-A0G-1999;
01-SEP-1999;
01-SEP-1999;
115-SEP-1999;
115-SEP-1999;
22-SEP-1999;
23-SEP-1999;
23-SEP-1999;
24-SEP-1999;
24-SEP-1999;
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232. 233. 236. 237. 239. 331. 331. 331. 331. 331. 331. 331. 3	52; Conservative 45; Mismatches 76; Indels 25; Gaps PLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFWAEEGCPLLIHQPSYSIINRW 60	VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKY-LDGIPEGSRASQGKSLSEGMLN	VNNIDMVRKLNDIAOERGOSLAQMALAWVLREGGEYGADTVTSALIGASSVEGLDNSLDS :: : : : : : : : :
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Search completed: September 13, 2001, 17:51:44 Job time: 1115 sec

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063277 mus musculu
028528 mustela put
014722 homo sapien
09x131 oryctolagus
09pwrl gallus gall
                                                                                                                           Opptm4 xenopus lae
Opptm5 xenopus lae
Ophtm5 thermoplasm
Opku57 vibrio chol
Ophph9 halobacteri
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023016 arabidopsis
005408 bacillus su
Q9rs66 deinococcus
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09ewf0 streptomyce
09pcq5 xylella fas
09h190 thermoplasm
09x265 thermotoga
02x265 thermotoga
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Q9i0u9 pseudomonas
                                homo sapien
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STRAIN-R127;
MEDLINE-97126810; PubMed-8971704;
Vrljic M., Sahm H., Eggeling L.;
"A new type of transporter with a new type of cellular function: L-lysine export from Corynobacterium glutamicum.";
Mol. Microbiol. 22:815-826(1996).
EMBL; X96471; CAA65325:1; -.
SROUENCE 209 AA; 22450 MW; 06549D44F0BC0100 CRC64;
    mns
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Q9hxk2 ps
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
Corynebacterium.
NCBI_TaxID=1718;
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Last annotation update)
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100.0%; Pred. No. 1.2e-75;
Live 0; Mismatches 0;
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Best Local Similarity
Matches 209; Conserv
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Q9pqd5
O59826
Q4328
Q64328
Q9f2z5
Q9f2z5
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                  version 4.5
- 2000 Compugen Ltd.
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                                                                                                            September 13, 2001, 17:51:50
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Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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sp_human:*
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Maximum DB seq length: 2000000000
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RESULT 046851

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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL049863; CAB42946.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oliver K., Harris D.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                           122 NIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDSLN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLNVN 121
                                                                                                                                                                                                                                                                                                                                                                     2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWV 61
                                                                                                                                   Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map the B Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL450223; CAC16515.1; -.
SEQUENCE 348 AA; 38441 MW; CFF77941897D9C1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 TVRRLRALNDIAARRGQSLAQMALAWALRD-----PRVTSLVIGASRPEQLEENVAALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
                                                                                                                                                                                                                                                                                          48.5%; Score 529; DB 2; Length 348; 54.3%; Pred. No. 6.2e-34; Live 29; Mismatches 54; Indels
 Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A. Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=A3(2);
James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) PUTATIVE ION CHANNEL SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 NPSFDDDELAEIDEYAVVDGDVDLWRRA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 NLEFSDAELEAIDEIS-HDAGINIWAKA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                         SEQUENCE FROM N.A.
STRAIN=A3(2);
MEDLINE=97000351; Pubmed=8843436;
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MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                                                                                                                                                                              Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSR----ASQGKSLSEG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 MLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seeger K.J., Harris D.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76037.1; -. 38832 MW; C70D4D43A3A57AFC CRC64;
                                                                                                                                                                             Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.5%; Score 529.5; DB 2; 51.4%; Pred. No. 5.6e-34; Live 38; Mismatches 51;
                                                                                                                     346 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 LDSLNNLEFSDAELEAIDEISHDAGINIWAKATD 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::|||| || || || || ::| ::| 312 VQALNNLTFSTKELAQIDQHIADGELNLWQASSD 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 AA
181 AELEAIDEISHDAGINIWAKATDSKTREN 209
                                                                                                                                                           Created)
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                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, PUTATIVE OXIDOREDUCTASE. SC7H9.06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 51.4%
Matches 110; Conservative
                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 AA;
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                ORF_0346.
Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-A3(2);
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242 DENIQKVRDLKSIADDLGVTRAQLALAWLLRQKG-----VSSVITGATKVNQIQDTVKA 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 VNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDS 179
256 LTKERLEQVQALNDLAQSRGQSLAQMALAWVLRERDD-KVQGITSALIGASRPQQIIENV 314
                                                                                                                                                                                                                                                                                                                                   White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Wakarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315 AA; 35156 MW; B7614CCEE22A7104 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
POTASSIUM CHANNEL, BETA SUBUNIT, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.0%; Score 283.5; DB 2 34.5%; Pred. No. 1.2e-14;
                                                                                                                                 315 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                             Created)
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Bacteria; Thermotogales; Thermotoga.
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                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                       MEDLINE=20036896; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001395; -
Pfam; PF00248; aldo_ket_red; 2.
Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 12, C
(TrEMBLrel. 12, I
(TrEMBLrel. 13, I
BETA SUBUNIT.
                              178 DSLNNLEFSDAELEAIDEI 196
                                             :|:|:|| || |:::
315 AALEHLKFTDEELIKIEKL 333
                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 286:1571-1577(1999).
EMBL; AE002063; AAF11861.1;
TIGR; DR2317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 LNNLEFSDAELEAIDEI 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                    Deinococcus radiodurans.
                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            radiodurans R1
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K+ CHANNEL, F
TM0313.
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01-NOV-1999
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Q9WYE9;
                                                                                                                                             Q9RS10;
                                                                                                                                Q9RS10
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Q9RS10
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                                                                                                                                                           EEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSR-ASQGKSLSEGMLNV 120
                                                                                                                                                                            WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQG--KSLSEGM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :||:|||| ||: : |||||||:::|
NTPIEETMGALKSALDSGKALYVGLSNYSAKET-EAAVLAAEKLGFKLLIHQPRYSMLDR 201
                                                                         Gaps
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                                                                                                   TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and nucleotide sequence of the beta-galactosidase gene from Lactococcus lactis ssp. lactis ATCC7962.";
Biotechnol. Lett. 19:179-183(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEE-GCPLLIHQPSYSIINR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                    121 NNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-ATCC7962;
Lee J.M., Chung D.K., Park J.H., Lee W.K., Chang H.C., Kim J.H.,
Lee H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee J.M., Chung D.K., Park J.H., Lee W.K., Chang H.C., Kim J.H., Lee H.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 334;
                                            Length 319;
                                                                       54; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactococcus lactis.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                il protein.
334 AA; 37574 MW; 0DA15BAA867CE2A3 CRC64;
34702 MW; D0114179AE30038B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 37.6 KDA PROTEIN.
Lactococcus lactis.
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                                          ; Score 449; DB 2;
; Pred. No. 1.1e-27;
25; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.2%; Score 438.5; DB 2
50.8%; Pred. No. 7.9e-27;
iive 35; Mismatches 52
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Pfam; PF00248; aldo_ket_red; 1.
Hypothetical protein.
                                          Query Match
Best Local Similarity 53.6%;
Matches 105; Conservative 29
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Best Local Similarity 50.8%
Matches 101; Conservative
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GNLDFDADELARIDKI 316
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MEDLINE=25504483; PubMed=11016950;
A MEDLINE=25504483; PubMed=11016950;
A Shukla H.D., Lasky S.P., Mahairas G.G., Thorson V., Sbrogna J.,
A Shukla H.D., Lasky S.R., Ballga N.S., Thorson V., Sbrogna J.,
A Shukla H.D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
A lam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
R. Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
R. EMBL, AEGOSOSS, AAG19415.1;
R. Interpro; IPRO01395;
R. Interpro; IPRO01395;
R. Richels Sci. U.S.A. 97:12176-12181(2000).
R. Pfam: PF00248; aldo_ket_red; 1.
SEQUENCE 336 AA; 37376 MW; 04C7676CED9BBE04 CRC64;
                                                                                                        255 SYLTEENFDVHDELDAVAGEVDATPAQTALAWLMHRDG------VTAPIVGARTVEQLTE 308
NRWVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYL--DGIPEGSRASQGKSLSE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 DTTARELMRTLNDLVADGLVHYLGASTLQPNAWRIARANELARAEGWEPFSVLQPRYNLV 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DTPLEETMYALRDIVASGKALYVGISSYGPEL, -TAEAAEFWAEEGC-PLLIHQPSYSII 57
                        GMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.8%; Score 238; DB 1; Length 336; 33.5%; Pred. No. 5e-11; Live 34; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium.
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halobacterium sp. (strain NRC-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 NIDAA-TIDLTDDQMARLTD 327
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Matches 67; Conservative
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PROBABLE OXIDOREDUCTASE.
YAJO2 OR VNG0998G.
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SEQUENCE FROM N.A.
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01-MAR-2001
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                                                                          Nelson K.E., Clayton R.A., 6111 S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
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Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
TIGR; TM0313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 WVEEPGDDGENLLQSAA----NNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ----GK 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloferax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 ------ERVEKEYAPLYEKYGMGLTTYSPLASGLLSGKYNNGIPEGSRLATFPQVRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.6%; Score 257; DB 1; Length 336; 32.1%; Pred. No. 1.6e-12; ive 40; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 319;
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                          319 AA; 36171 MW; E4B1F32F41719B39 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
0xiDOREDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                       24.5%; Score 267; DB 2; 33.8%; Pred. No. 2.4e-13; iive 43; Mismatches 70
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                                         STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed-10360571;
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PRINTS; PR00069; ALDKETRDTASE.
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Matches 67; Conservative
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Kim K.S., Farrand S.K.;
"Ti plasmid-encoded genes responsible for catabolism of the crown gall opine mannopine by Agrobacterium tumefaciens are homologs of the Tregion genes responsible for synthesis of this opine by the plant tumor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 PEGKTQLDQVRQISKIAEQIGATPSQLALAWTLKN-----PYVSTTILGASKPEQI--- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 PMEEVVRAFTQLIQDGKAFYWGTSEWS-AFEIEHAHHIATKYNLIAPVADQPQYNYLTRD 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL--LIHQPSYSIINRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 HFE-----KDLLPLQQIYGYGATVWSPLKSGILTGKYNDGIPEGSRLSTTFTSLAGQLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----NNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66; Indels
                                                                                                                                                                                                   STRAIN=972H-;
Wood V., Rajandream M.A., Barrell B.G., Rieger M.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AL023590; CAA19066.1;
                                                                                                                                                                                                                                                                                                                   344 AA; 38430 MW; A57A25E60B05CAE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 AA; 38846 MW; 21D4074605E80EB6 CRC64;
                                                             Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 20.9%; Score 227.5; DB 3; Best Local Similarity 32.8%; Pred. No. 3.5e-10; Matches 67; Conservative 37; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.5%; Score 213; DB 2; 32.5%; Pred. No. 5.1e-09; iive 35; Mismatches 66;
                                            Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
  PUTATIVE POTASSIUM CHANNEL SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 178:3275-3284(1996).
EMBL; AF242881; AAB07785.1; -.
Interpro; IRRO01395; -.
Pfam; PF00248; aldo_ket_red; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 LDSLNNLEFSD----AELEAIDEI 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 VENVKAVEFIDKLTPEILKKIDEI 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=15955;
MEDLINE=96236046; PubMed=8655509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agrobacterium radiobacter.
Plasmid pTi15955.
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Best Local Similarity 32.55
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobiaceae; Rhizobium.
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                 Ionic channel
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Q44328;
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2
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Matture 406:151-159(2000).

Matture 406:151-159(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 LSEGMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Gaps
                                                                                           Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EECOC1A28EF9B7BF CRC64;
01-MAR-2001 (TrEMBLrel. 16, Last annotation update) VOLTAGE-GATED POTASSIUM CHANNEL BETA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.8%; Score 237.5; DB 2; 33.7%; Pred. No. 6.8e-11; ive 31; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                            MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR00069; ALDKETRDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 AA; 42793 MW;
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Best Local Similarity 33...
"hea 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 LDNSLDSLNNLEFSDA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 LKENLRALQVVAALDA 376
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                                                                 Xylella fastidiosa
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                 NCBI_TaxID=2371;
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01-AUG-1998 (
01-MAY-2000 (
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                         186
                                                  53 SYSIINRWVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYL--DGIPEGSRASQG 110
                                                                                                    165
                                                                                                                                                                                                                                                                                                                                                                                                                                           Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hinfagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Relzer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PA01, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGI-PEGSRASQGKSLSEGMLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 PQAEAACARYVALAREHGLEPAQMALAYVT----SRPFVTSNIIGATSLEQLETNLGS 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIH-QPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
2 TPLEETMYALRDIVASGKALYVGISSY------GPELTAEAAEFMAEEGCPLLIHQP
                       134 TPLEETMEALDTLVROGKVRYIGCSNFTGWOIMKALGISEKDKRORFVSQQ----IH--
                                                                 111 KSL----SEGMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALI
                                                                                                                             240 WTEPPVRDEERLWNI-----VDTLLSVADGRGVSAAQVALAWLI-----GRKAVTSIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 FE-----VGLAEIAIREQCGLLAYSPAAFGMLSGKYADGARPANARISLYSRFTR-YIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 VNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38644 MW; 6866B69139E62508 CRC64;
                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 19.3%; Score 211; DB 2; Le
Best Local Similarity 33.0%; Pred. No. 7e-09;
Matches 66; Conservative 33; Mismatches 85;
                                                                                                                                                                                                                                                  345 AA
                                                                                                                                                                       289 GGRTEAQFKDNL-AAADLQLSAEERKRLDDVS 319
                                                                                                                                                       GASSVEQLDNSLDSLNNLEFSDAELEAIDEIS 197
                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=PAO1;
MEDLINE=20437337; Pubmed=10984043;
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PRINTS; PR00069; ALDKETRDTASE.
ProDom; PD002680; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL, AE004857, AAG07822.1; -.
InterPro; IPR001395; -.
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                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, PROBABLE OXIDOREDUCTASE.
                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas
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136 TPFEEIWQAIDVLVQQGKILYAGSSNFPGYKIAQANEIAARRGGTIGLVSEQCLYNLAER 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 TKTREQIQAYEDLLDKHGLQPGEAALAWLLTRPG-----VTGPIVGPRTQEQLDSALRA 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.NCBI_TaxID=1902;
                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 330;
                                                                                                                                                                                                                                                                                                                                  Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81; Indels
                                                                                                                                                                                                                                             Seeger K.J., Harris D.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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32.0%; Pred. No. /...
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                                               01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, PUTATIVE OXIDOREDUCTASE.
                               01-MAR-2001 (TrEMBLrel. 16,
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L-ELELSEELLTSLDEI 317
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PRELIMINARY;
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Best Local Similarity
Matches 63; Conserv
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SEQUENCE FROM N.A.
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SEQUENCÈ FROM N.A.
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SEQUENCE FROM N.A.
STRAIN-A3(2);
                                                                                                                                                                         NCBI_TaxID=1902;
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Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
the B Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL138852; CAB72221.1; -.
InterPro; IRR001395, -.
Pfam; PF00048; aldo_ket_red; 2.
Pranty: PR00069; ALDKETRDTASE.
SEQUENCE 336 AA; 37060 MW; C66860A31C9BB62C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 19.3%; Score 210.5; DB 2; Length 336; Best Local Similarity 33.0%; Pred. No. 7.4e-09; Matches 63; Conservative 34; Mismatches 59; Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIH-QPSYSIINR 59
                                                                   STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
Brown S.P., Harris D.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                              STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
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us-09-105-117i-2.rsp A 2 (Lyo E)

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 13, 2001, 17:52:15; Search time 15.26 Seconds (without alignments) 484.875 Million cell updates/sec Run on:

US-09-105-1171-2 1091 Title: Perfect score: Sequence:

1 DIPLEETMYALRDIVASGKA.......SHDAGINIWAKATDSKTREN 216

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

93435 seqs, 34255486 residues Searched:

93435

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES		
Result No.	Score	Query	Length	BB	ID	Description	
1	225	20.6		Н	₹.	escherichi	a
7	193	17.7	326	Н	YDJG_ECOLI		ದ
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4	180.5	16.5		Н	TAS_ECOLI		æ
2	178	16.3		-	YAKC_SCHPO	Q09923 schizosacch	ч
9	161.5	•		Н	YM98_MYCTU	Q50668 mycobacteri	٠,
7	159.5			Н	AR72_HUMAN		c
80	157.5	4		Н	AR73_HUMAN	homo	c
6	156.5	14.3		Н	AR71_RAT	rattu	>
10	152.5	4		Н	STCV_EMENI	_	
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32	90.5	8.3	1252	7	PIG2_HUMAN	P16885 homo sapien	c
33	89.5	8.5	379	~4	DCOP_TRIHA	Q12709 trichoderma	æ

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Gaps

26;

60 WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ-----GKSL 113

Dp δ

δy

1 DIPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIH-QPSYSIINR 59

Query Match 20.6%; Score 225; DB 1; Length 324; Best Local Similarity 31.9%; Pred. No. 4.2e-11; Matches 60; Conservative 39; Mismatches 63; Indels

P45450 synechocyst 009332 drosophila P26690 glycine max P42259 natronomona Q12397 emericella Q01570 pavlova lut O13764 schizosacch 067139 aquifex aeo 004974 lycopersico Q92020 mus musculu P49378 kluyveromyc Q92d08 rickettsia	95	AA. (te)	<pre>Rel: 37, Last annotation update) OXIDOREDUCTASE IN PGPA-ISPA INTERGENIC REGION. oli. teobacteria; gamma subdivision; Enterobacteriaceae;</pre>		A., Perna N.T., Burland V., , Rode C.K., Mayhew G.F., Goeden M.A., Rose D.J.,	Escherichia coli K-12.";	SEQUENCE FROM N.A. SEQUENCE FROM N.A. Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Mamath A., Oefner P., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases. -: SIMIIARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ilab.sib.ch).	LT_INIT. _INIT. ductase. HYDROGEN BOND DONOR (PROBABLE). 0B69E09F2BEDF9B1 CRC64;
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8 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT 1	_ECOLI YAJO_ECOLI P77735; 01-NOV-1997 15-DEC-1998	15-DEC-1998 (Rel HYPOTHETICAL OXI YAJO. Escherichia coli	ESCHELICHIA. NCBI_TAXID=562; [1] SEQUENCE FROM N	STRAIN=K12 / MG1655; MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., KRiley M., Collado-Vides J., Glasner J.D., Rc Gregor J., Davis N.W., Kirkpatrick H.A., Goc	Mau B., Shao Y.; "The complete genome Science 277:1453-147	SECULAR SECULATION N.A. Roberts D., Allen Duncan M., Federsp Lew H., Lin D., Na Submitted (JAN-199	This SWISS-PR between the the European use by non- modified and entities requ or send an em	EMBL; AE000148; AAC73522.1; ALT_INIT. EMBL; U82664; AAB40175.1; ALT_INIT. Ecodene; EG13611; yajo. Hypothetical protein; Oxidoreductase. ACT_SITE 127 127 HYDROGEN-B SEQUENCE 324 AA; 36420 MW; 0B69E09F
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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    ----DAEKELLPYCEKQGISFIPYFPLASGLLTGKFTQDTVFDDFR--*CDKPQFQGETFI 239
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15-UUL-1999 (Rel. 36, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
HYPOTHETICAL OXIDOREDUCTASE IN NATB-RAPJ INTERGENIC REGION (ORFC).
                                                                                                                                                                                                                    254 --IDMLEQWQPLCARYQCTIPTLALAWILKQ-----SDLISILSGATAPEQVRENVAAL
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Hypothetical protein; Oxidoreductase.

ACT_SITE 127 127 HYDROGEN-BOND DONOR (PROBABLE).

SEQUENCE 310 AA; 34800 MW; C06BF4195D25C91C CRC64;
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Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
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Bacillus/Staphylococcus group; Bacillus.
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SEQUENCE OF 1-268 FROM N.A.
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InterPro; IPR001395; -.
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SEQUENCE FROM N.A.
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P46905;
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Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T.,
Ikemoto K., Inada T., Isono K., Itoh T., Kanai K., Kasai H.,
Kashimoto K., Kim S., Kimura S., Kitagawa M., Attakawa M., Makino K.,
Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y.,
Masudoto H., Nishio Y., Oshima T., Salto N., Sampel G., Seki Y.,
Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                240 YKES-DENDAQIAERLIGVSEELGATRAQVALAWLLSKPG-----IAAPIIGTSREEGL 292
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattiner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                              SEGMLNVNNIDMVRKLNDIAQERGOSLAQMALAWVLREQGEYGADTVTSALIGASSVEQL
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL OXIDOREDUCTASE IN ANSA-RND INTERGENIC REGION
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31.0%; Pred. No. 1.6e-08;
tive 40; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 AA.
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Best Local Similarity
Matches 62; Conserv
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P77256;
15-JUL-1998 (
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Escherichia.
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SEQUENCE
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111 KSLSEGMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSV 170
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                                   1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRW
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340 AA; 37710 MW; A4A9686A70968F06 CRC64;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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01-FFB-1996 (Rel. 33, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
01-FBB-1996 (Rel. 37, RDA PROTEIN C1F7.12 IN CHROMOSOME
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26.8%; Pred. No. 2.7e-07;
Live 42; Mismatches 88;
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                                                                                                                                                        InterPro; IPR001395; -.
Pfam; PF00248; aldo_ket_red; 1.
Hypothetical protein; Oxidoreductase.
ATSITE 126
EQUENCE 340 AA; 37710 MW: A4A96R
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Best Local Similarity
Matches 55; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                 YAKC_SCHPO
Q09923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-972;
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                                                            268
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=B/R / WU3610;
MEDLINE-B/R / WU3610;
Timms A.R., Bridges B.A.;
"Reversion of the tyrosine ochre strain Escherichia coli WU3610 under stravation conditions depends on a new gene tas.";
Genetics 148:1627-1635(1998).
-: SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGI-PEGSRAS-----QG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 SFE-----VGLAEVSQYEGVELLAYSCLGFGTLTGKYLNGAKPAGARNTLFSRFTRYSG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLDTLDALAEYQRAGKIRYIGVSNETAFGVMRYLHLAD---KHDLPRIVTIQNPYSLLNR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 41; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-KIZ / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                        346 AA.
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38499 MW;
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EMBL; Y14609; CAA74961.1; -.
HSSP; P14550; ZALR.
                                                                                         181 NNLEFSDAELEAIDEI 196
                                                                                                                                                  -NIELTEDEVNFISDI 308
                                                                                                                                                                                                                                                                                                        STANDARD;
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InterPro; IPR001395;
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Q46933;
15-JUL-1998 (Rel. 3(
15-JUL-1998 (Rel. 31)
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Best Local Simi.
Matches 63; (
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SEQUENCE
                            240
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AKR7A2 OR AFAR OR AKR7.
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                                                                            SEQUENCE FROM N.A.
                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                           TISSUE-Brain;
                                                                                           TISSUE=Liver;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                      Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                             Goldon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Taylor K., Whitehead S., Barrell B.G., Squres S., Sqares R., Sulston J.E. Techpering the blology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 MYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWVEEPGDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 RKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDSLNNLEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 HYDROGEN-BOND DONOR (BY SIMILARITY).
34986 MW; FF071A48B745B8E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 323;
                                                                                                                                                                                                                                                                                                                               -! SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AR72_HUMAN STANDARD; PRT; 330 AA.
043488; 075749;
15-JUL-1999 (Rel. 38, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AFLATOXIN B1 ALDEHYDE REDUCTASE 1 (EC 1.-.-.) (AFB1-AR 1)
(ALDOKETOREDUCTASE 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.8%; Score 161.5; DB 1;
32.8%; Pred. No. 5.4e-06;
Live 29; Mismatches 71;
                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tuberculist; Rv2298; -.
Hypothetical protein; Oxidoreductase.
ACT_SITE 117 117 117
SEQUENCE 323 AA; 34986 WW; FF071A
            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence u
30-MAY-2000 (Rel. 39, Last annotation;
HYPOTHETICAL 34.9 KDA PROTEIN RV2298.
                                                                                                                                                                    MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 277163; CAB00973.1; -.
                                                                            Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61; Conservative
                                                               RV2298 OR MTCY339.12C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=1773;
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                                                                                                                                                        STRAIN-H37RV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CAN METABOLIZE THE AFLATOXIN BI (AFB1) PROTEIN-BINDING DIHYDRODIOL BY FORMING NONBINDING AFB1 DIALCOHOL. COULD BE INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGENIC EFFECTS OF AFLATOXIN B1. ACTS AS A 2-CARBOXYBENZALDEHYDE
                                                                                                                                                                                                                                                                                Ireland L.S., Harrison D.J., Neal G.E., Hayes J.D.;
"Molecular cloning, expression and catalytic activity of a human AKR7 member of the aldo-keto reductase superfamily: evidence that the major 2-carboxybenzaldehyde reductase from human liver is a homologue of rat aflatoxin Bl-aldehyde reductase.";
Biochem. J. 332:21-34(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ---GKSLSEGM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 LN-----VNNIDMVRKLNDIAQ-ERGQSLAQMALAWVLRE---QGEYGADTVTSALIG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Praml C., Savelyeva L., Perri P., Schwab M.; "Cloning of the human aflatoxin B1-aldehyde reductase gene at 1p35-1p36.1 in a region frequently altered in human tumor cells."; cancer Res. 58:5014-5018(1998).
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 VE-----TELFPCLRHFGLRFYAYNPLAGGLLTGKYKYEDKDGKQPVGRFFGNSWAETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5; DB 1; Length 330;
8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDROGEN-BOND DONOR (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A -> T (IN REF. 1).
3BBFB7ED0CAF4D54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 159.5;
Pred. No. 8e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 ASSVEQLDNSLDSLNNLEFSDAELEAIDEISH 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 MSSLEQLEQNLAATEEGPLEPAVVDAFNQAWH 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99040634; Pubmed-9823300;
                                                                                                                                                                                                                                                     MEDLINE=98244807; PubMed=9576847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF026947; AAC52104.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36618 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.6%; 27.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112
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                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        133 RNRYWKEHHFEGIALVEKALQAAYGASAPSMTSATLRMMYHHSQLQGAHG----DAVILG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VE-----TELFPCLRHFGLRFYAFNPLAGGLLTGKYKYEDKNGKQPVGRFFGNTWAEMY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LN-----VNNIDMVRKLNDIAQ-ERGQSLAQMALAWVLRE---QGEYGADTVTSALIG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ---GKSLSEGM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADOSPEGCGSFWGTLGPGADCCFPS (IN REF.
                                                                                                                                                                       Knight L.P., Primiano T., Groopman J.D., Kensler T.W., Sutter T.R., "cDNA cloning, expression and activity of a second human aflatoxin B1-metabolizing member of the aldo-keto reductase superfamily,
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYDROGEN-BOND DONOR (PROBABLE)
                         AR73_HUMAN STANDARD; PRT; 331 AA.
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
AFLATOXIN B1 ALDEHYDE REDUCTASE 2 (EC 1....) (AFB1-AR 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> D (IN REF. 1).
-> A (IN REF. 1).
B9C32C33C7102AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 157.5; DB 1;
Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E -> D (IN REF.
V -> M (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30; Mismatches
                                                                                                                                          SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                              MEDLINE-99315412; PubMed-10383892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 2 N E
                                                                                                                                                                                                            Carcinogenesis 20:1215-1223(1999).
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF040639; AAD02195.1; -. EMBL; AL035413; CAB72322.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PR00069; ALDKETRDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37206 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.48;
27.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215
323
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL035413; CAB72
InterPro; IPR001395;
                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215
323
331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase
                                                                                                                                                     TISSUE=Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS;
                                                                                                                                                                                                  AKR7A3.
                                                                                    AKR7A3
        RESULT 8
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                                    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carcinogenesis 20:1215-1223(1999).
-1- FUNCTION: CAN METSABOLIZE THE AFLATOXIN B1 (AFB1) PROTEIN-BINDING
-1- FUNCTION: CAN METSABOLIZE THE AFLATOXIN B1 (AFB1) DIALCOHOL. COULD BE
INVOLVED IN PROTECTION OF LIVER AGAINST THE TOXIC AND CARCINOGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Knight L.P., Primiano T., Groopman J.D., Kensler T.W., Sutter T.R.; "cDNA cloning, expression and activity of a second human aflatoxin B1-metabolizing member of the aldo-keto reductase superfamily,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-FISCHER 344; TISSUE-Liver;
MEDLINE-94052160; PubMed-8234296;
Ellis E.M., Judah D.J., Neal G.E., Hayes J.D.;
"An ethoxyquin-inducible aldehyde reductase from rat liver that metabolizes aflatoxin B1 defines a subfamily of aldo-keto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93364879; PubMed=8395332; MEDLINE=93364879; PubMed=839532; Mey G.D., Judah D.J., Neal G.E.; Resistance to aflatoxin Bl is associated with the expression on ovel aldo-keto reductase which has catalytic activity towards cytotoxic aldehyde-containing metabolite of the toxin."; Cancer Res. 53:3887-3894(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 156.5; DB 1; Length 327; Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- INDUCTION: BY THE PHENOLIC ANTIOXIDANT ETHOXYQUIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PROBABLE)
                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
AFLATOXIN BI ALDEHYDE REDUCTASE (EC 1...) (AFB1-AR).
AKR7A1 OR AFRAR.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYDROGEN-BOND DONOR (PROB. 7427F3383AC190FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 6-17; 89-97; 156-184; 232-246 AND 250-274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reductases.";
Proc. Natl. Acad. Sci. U.S.A. 90:10350-10354(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raymackers J., Anderson L.;
Submitted (NOV-1994) to the SWISS-PROT data bank.
                                                                                                                                                                                                                          327 AA.
167 ASSVEQLDNSLDSLNNLEFSDAELEAIDEISH 198
                                                         289 MSSLEQLEQNLAAAEEGPLEPAVVDAFNQAWH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver;
MEDLINE=99315412; PubMed=10383892;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.3%;
26.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFFECTS OF AFLATOXIN B1
                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              601
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SEQUENCE
                                                                                                                                                                                                                          AR71_RAT
                                                                                                                                                                                                                                                               P38918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKR7A3.
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117 MLNVNNID-----MVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVE 171
                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001395; -. Pfam; PF00248; aldo_ket_red; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YOKF_BACSU STANDARD; F
P54569;
01-0CT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 H
33857 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.7%;
25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X56267; CAA39708.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 25.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CV. WHITE BURLEY;
van der Zaal E.J.;
                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 SSVEQLDNSL 177
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292 TKIENLNQNM 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S16390; S16390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase
                                                                                                                                                                                                                                                            A115_TOBAC
P40691;
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SEOUENCE
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                                                                                        115 TPIEETLOACHHVHQEGKFVELGLSNYVSWEVAEICTLCKKNGWIMPTVYQGMYNAITRQ 174
                                                                                                                                      61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ---GKSLSEGM 117
                                                                                                                                                              118 L------NVNNIDMVRK-LNDIAQERGOSLAQMALAWVLRE---QGEYGADTVTSALIG 166
                                                                                                                                                                                                                                                                             229 MDRYWKEEHFNGIALVEKALKTTYGPTAPSMISAAVRWMYHHSOLKGTQG----DAVILG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSL---SEG 116
       Gaps
                                             TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINRW 60
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Keller N.P., Adams T.H., Leonard T.J.;
Twenty-five corequiated transcripts define a sterigmatocystin gene cluster in Aspergilus nidulans.
Proc. Natl. Acad. Sci. U.S.A. 93:1418-1422(1996).
--- FUNCTION: MAY BE INVOLVED IN THE DEHYDRATION OF 5'-
HYDROXYAVERANTIN TO FORM AVERUEIN.
--- PATHWAY: STERIGMANTOCYSTIN BIOSYNTHESIS.
--- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emericella nidulans (Aspergillus nidulans).
Bukaryota; Fungi, Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; Emericella.
NCBI_TAXID=5072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PUTATIVE STERIGMATOCYSTIN BIOSYNTHESIS DEHYDROGENASE STCV
    Indels
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94;
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                                                                                                                                                                                                                                                                                                                           167 ASSVEQLDNSLDSLNNLEFSDAELEAIDE----ISHD 199
                                                                                                                                                                                                                                                                                                                                                       285 MSSLEQLEQNLALVEGPLEPAVVDAFDQAWNLYAHE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.0%; Score 152.5; DB 27.0%; Pred. No. 3.6e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 AA
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Mismatches
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MEDLINE-96202293; PubMed-8643646;
  37;
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43548 MW;
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    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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ACT_SITE 148
SFONENCE 387 AA;
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57;
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    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Nicotiana.

NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
                          --SPYVFPVIGCRTVE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 EPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLN--- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----VINIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subjitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
-!-INDUCTION: BY AUXIN.
-!-SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDROGEN-BOND DONOR (PROBABLE).
C4417DA852613360 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 1; Length 307; 4.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59; Indels
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-UL-1998 (Rel. 36, Last annotation update)
AUXIN-INDUCED PROTEIN PCNT115.
                                                                                                                                                                                                                                                                                                                      307 AA.
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Pred. No. 4.
                                                                                                                           305 QLEANITSL-GVELSDEEIYEIEDTIPFDVG 334
                                                                                      172 OLDNSLDSLNNLEFSDAEL-EAIDEISHDAG 201
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"Cloning and sequencing of a 36-kb region of the Bacillus subtilis genome between the gnt and iol operons.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.4%; Score 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Licellus.
Bacillus/Staphylococcus group; Bacillus.
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                                                                                                                                                                                                                                                                                    MEDLINE=97443988; PubMed=9298659;
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Pfam; PF00248; aldo_ket_red; 1.
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P80874; 007583;
01-NOV-1997 (Rel. 35, Created)
15-UUL-1998 (Rel. 36, Last seque
15-JUL-1998 (Rel. 36, Last anno
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35168 MW;
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P23457; 1LWI.
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                                            DNA Res. 2:61-69(1995).
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310 AA;
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Best Local Similarity
Matches 49; Conserv
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                                                                                                                                                                                                                                         SEQUENCE OF 1-20.
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SEQUENCE
                                                                                                                                                                             Bacillus
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GS69_BACSU
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                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                      the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 PGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLS-EGMLNVNN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
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                                                                                                                                                                                                                                     Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S., Sabto T., Takeuchi M., Sabto T., Takeuchi M., Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL OXIDOREDUCTASE IN ANSR-BMRU INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.4%; Score 146; DB 1; Length 306; 25.5%; Pred. No. 8.9e-05;
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                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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VY-2000 (Rel. 39, Last annotation update)

PROTEIN (VEGETATIVE PROTEIN 147) (VEG147)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D84432; BAA12638.1; -.
EMBL; Z99116; CAB14294.1; -.
Subtilist; BG11761; YqkF.
InterPro, IPR001395; -.
Pfam: PF00248; aldo_ket_red; 1.
Hypothetical protein; Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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MEDLINE=96093926; PubMed=7584049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequ
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 AA; 34717 MW;
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                                                                                                                                                                                                                   JH642;
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                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                    Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                     NCBI_TaxID=1423;
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Matches 50;
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P46336;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Hecker M.;
"First steps from a two-dimensional protein index towards a response-
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[2]
SEQUENCE FROM N.A.
STRAIN=168 / BGSC1A1;
STRAIN=16, Yoshida K.-I.;
"Organization and transcription of the myo-inositol operon, iol, of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulation map for Bacillus subtilis.";
electrophoresis 18:1451-1463(1997).
-!- PATHWAY: MYO-INOSITOL CATABOLISM.
-!- PATHWAY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYDROGEN-BOND DONOR (PROBABLE)
A870F226F8684867 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83; Indels
                                                                                                                                                                                                                 Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 9e-05;
37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last annotation update)
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            REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "First steps from a two-dimensional protein index towards a response-
regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-1463(1997).
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, LIMITATION AND OXYGEN LIMITATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
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                                                                                                                                                         Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S., Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                     Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
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82BC24D46E4994D0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 SLD----SLNNLEFSDAELEAIDEISHDAGINIWAKAT 209
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NORSOLORINIC ACID REDUCTASE (EC 1.1.1.-).
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EMBL; 299109; CAB12792.1; -.
HSSP; P23457; ILWI.
SubtiList; BG13020; yhdN.
Pfam; PF00248; aldo_ket_red; 1.
Oxidoreductase; Heat shock.
ACT_SITE 125 HYDR
CONFLICT 25 25 G ->
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97443988; PubMed=9298659;
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                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-25.
ACBI_TaxID=1423;
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"First ster
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MEDLINE=96156784; PubMed=8593042;
Cary J.W., Wright M., Bhatnagar D., Lee R., Chu F.;
"Molecular characterization of an Aspergillus parasiticus
dehydrogenase gene, norA, located on the aflatoxin biosynthesis gene
cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLNV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYDROGEN-BOND DONOR (POTENTIAL). 758B8187187BF5B0 CRC64;
                                                                                                                                                                                                                                    -i- PATHWAY: AFLATOXIN BIOSYNTHESIS.
                                                                                                                                                                                                        62:360-366(1996).
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388 AA; 43751 MW;
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GenCore version 4.5
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OM protein - protein search, using sw model

September 13, 2001, 17:34:55 ; Search time 25.14 Seconds
(without alignments)
654.483 Million cell updates/sec Run on:

US-09-105-1171-2 1091 1 DTPLEETMYALRDIVASGKA.....SHDAGINIWAKATDSKTREN 216 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database

pir1:*
pir2:*
pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	hypothetical prote -	_=	probable ion chann	oxidoreductase yug	probable potassium	K+ channel, beta s	oxidoreductase [im	probable oxidoredu	voltage-gated pota	probable potassium	probable NAD(P)H-d	probable oxidoredu	mocA protein [impo	probable oxidoredu	probable potassium	alpha-dendrotoxin-	potassium channel	RCKbeta2 protein -	probable oxidoredu	potassium channel	potassium channel	K+ channel beta-su	hypothetical prote	oxidoreductase Tas	aryl-alcohol dehyd	potassium channel	sugar-phosphate de	hypothetical prote	aldo/keto reductas
SUMMARIES	QI.	G65086	E85959	T35337	B86873	A75289	H72391	T44988	C84256	F82815	T41659	E85538	C64771	T44934	B83093	T07394	A53131	866502	845312	F83170	866503	I59393	I55463	D85787	C82294	D84315	T52133 ·	F69978	C64937	E75296
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dЯ	Query Match I	48.5	 	41.2	33.5	26.0					20.9				19.3	19.2	19.2	19.1	19.1	18.9	18.8	18.8	18.8		•	•	•	17.8	•	17.7
	Score	529.5	526.5	449	366	283.5	267	257	238	237.5	227.5	225	225	213	211	509	209	208	208	206.5	205	202	205	197.5	197	196		194.5	193	193
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hypothetical prote probable oxidoredu	sugar-phosphate de sugar-phosphate de	ion channel homolo hypothetical prote	hypothetical prote	oxidoreductase, al	auxin-induced prot	probable oxidoredu	probable potassium	potassium channel	probable oxidoredu	oxidoreductase, al	hypothetical prote	hypothetical prote
S75995 H83328	E82644 D82644	B69755 F85935	C65066	F72218	T12582	562584	T03384	S68409	H83427	H72307	861978	C86176
77	77	7 7	~	~	7	7	7	7	7	~	7	7
314	329 362	310 346	346	274	338	340	326	404	323	333	342	453
17.5	17.1 16.8	16.7	16.5	16.5	16.4	16.3	16.2	16.0	15.6	15.3	15.1	15.0
191 189	186.5 183.5	182.5	180.5	180	178.5	178	177	174.5	170	167	165	163.5
30	32 33	34 35	. 36	37	38	39	40	4.1	42	43	44	45

ALIGNMENTS

RESULT

G65086 hypothetical protein b3001 - Escherichia coli (strain K-12) C.Species: Escherichia coli C.Species: Escherichia coli C.Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 18-Feb-2000 C.Accession: G65086 C.Accession: G65086 R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617 A;Reference number: A64720; MUID:97426617 A;Accession: G65086 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-346 < ABLAT> A;Cross-references: GB:AE000382; GB:U00096; NID:92367182; PIDN:AAC76037.1; PID:917893 A;Experimental source: strain K-12, substrain MG1655	C, Superrainity: itssion yeast pylluovine * denyulogenase
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ä Gaps Length 346; Indels Ouery Match 48.5%; Score 529.5; DB 2; Best Local Similarity 51.4%; Pred. No. 3.1e-34; Matches 110; Conservative 38; Mismatches 51;

143 NTPMEETASALAHAVQSGKALYVGISSXSPERTQKMVELLREWKIPLLIHQPSYNLLNRW 202 1 DIPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRW 60 Q δ qq

117 MLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNS 176 q δ

177 LDSLNNLEFSDAELEAIDEISHDAGINIWAKATD 210 δλ

::|||| || || || :| :| :| 312 VQALNNLTFSTKELAQIDQHIADGELNLWQASSD 345 g

RESULT 2
E85959
probable reductase 24354 [imported] - Escherichia coli (strain 0157:H7)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: E85959
F;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, Iiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Inature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551

D.J.; May K.; Apoda

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83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A75289
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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Matches 68;
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A:Accession: E85959
A;Status: preliminary
A:Molecule type: DNA
A:Molecule type: DNA
A:Mosdues: 1-346 <STO>
A:Cross references: GB:AE005174; NID:g12517567; PIDN:AAG58137.1; GSPDB:GN00145; UWGP:Z43
A:Experimental source: strain 0157:H7, substrain EDL933
C:Genetics:
A:Gene: Z4354
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: T35337
R; Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, May 1999
R; Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, May 1999
A; Reference number: Z21575
A; Reference number: Z21575
A; Reference number: Z3337
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-319
A; Coss-references: EMBL:AL049863; PIDN:CAB42946.1; GSPDB:GN00070; SCOEDB:SC5H1.21c
A; Experimental source: strain A3(2)
A; Genetics: SCOEDB:SC5H1.21c
C; Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                   3;
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C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 18-Feb-2000
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                                                                                                                                                                                                                                                                                   15;
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                                                                                                                                                                                                                                          Length 346;
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Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                    Ouery Match
48.3%; Score 526.5; DB 2;
Best Local Similarity 50.9%; Pred. No. 5.3e-34;
Matches 109; Conservative 39; Mismatches 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::|||| || || || || :| :| :| 312 VQALNNLTFSTEELAQIDQHIADGELNLWQASSD 345
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A;Cross-references: GB:AE002063; GB:AE000513; NID:g6460121; PIDN:AAF11861.1; PID:g646
A;Experimental source: strain Rl
                                                                                                                                                                                                                                                                              J.,
oxidoreductase yugB [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C; Species: Lactococcus lactis subsp. lactis c) Lactococcus lactis subsp. lactis (C; Species: Lactococcus lactis subsp. lactis (C; Species: Lactococcus lactis subsp. lactis (C; Accession: B86873 R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Genome Res. in press, 2001 A; Title: The complete genome sequence of the lactic acid bacterium. A; Reference number: A86625 A; Accession: B86873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probable potassium channel, beta subunit - Deinococcus radiodurans (strain R1) probable potassium channel, beta subunit - Deinococcus radiodurans (strain R1) c; Species: Deinococcus radiodurans (3-bec-1999 #sequence_revision 03-bec-1999 #text_change 17-Mar-2000 c; Date: 03-bec-1999 #sequence_revision 03-bec-1999 #text_change 17-Mar-2000 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vanathevan, J.J.; Lan, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. science 286, 1571-1577, 1999 A;Fitle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RA;Reference number: A75250; MUID:20036896
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A Molecule type: DNA
A Molecule type:
A Molecule type:
C Molecu
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143 NTPIEETMGALKSALDSGKALYVGLSNYSAKET-EAAVLAAEKLGFKLLIHQPRYSMLDR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQG--KSLSEGM 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A;Map position: 1
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.0%; Score 283.5; DB 2;
llarity 34.5%; Pred. No. 5.7e-15;
Conservative 40; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.5%; Score 366; DB 2; 54.6%; Pred. No. 1.7e-21;
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R1.

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probable oxidoreductase [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: C84256
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
Jung, K.H.; Alam, W.; Frettas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Accession: C84256
A;Status: preliminary
A;McCession: C84256
A;Status: preliminary
A;McCession: C84256
A;Genome A;McCession: C84266
A;Genome A;McCess
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A;Cross-references: GB:AE004437; NID:g10580553; PIDN:AAG19415.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYLTEENFDYHDELDAVAGEVDATPAQTALAWLMHRDG------VTAPIVGARTVEQLIE 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 GMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDN 175
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                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                 1 DIPLEETMYALRDIVASGKALYVGISSYGPEL--TAEAAEFMAEEGC-PLLIHQPSYSII 57
                                                                                                                                                                                                                                                                                                                                                                                                                 1 DTPLEETMYALRDIVASGKALYVGISSYGPEL--TAEAAEFMAEEGC-PLIHQPSYSII
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                                                                                                                        Length 336;
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A;Note: expressed during exponential growth
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: yajO2
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.8%; Score 238; DB 2;
33.5%; Pred. No. 2.3e-11;
tive 34; Mismatches 81;
                                                                                                                        ch 23.6%; Score 257; DB 2;
1 Similarity 32.1%; Pred. No. 7.5e-13;
67; Conservative 40; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 NLEAA-TIDLTDEQVDRLTGAKPDPYVGL 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 33.5%
Matches 67; Conservative
                                                                                                                        Query Match
Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics
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A;Molecule type: DNA
A;Residues: 1-319 <ARN>
A;Cresidues: 1-719 <ARN>
A;Cresidues: 1-719 <ARN>
A;Cresidues: 1-719 <ARN>
A;Cresiduental source: strain MSB8
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Thermotoga maritima
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C; Accession: #72391
R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sed
A;Reference number: A72200; MUID:99287316
A;Accession: H72391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase [imported] - Haloferax volcanii megaplasmid pHV3
C;Species: Haloferax volcanii
C;Species: Tabault, J.C.; St Jean, A.; Chan, C.C.Y.; Allard, G.; Charlebois, R.L. submitted to the EMBL Data Library, March 1997
A;Poscription: Hereditary instability of the megaplasmid pHV3, and filamentation in the A;Reference number: 222886
A;Accession: T44988
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                          SLSE-GMLNVNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WVEEPGDDGENLLQSAA----GK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEG-CPLLIHQPSYSIINR 59
                             120 VNNIDMVRKLNDIAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.5%; Score 267; DB 2; Length 319; 33.8%; Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                             K+ channel, beta subunit - Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: TM0313
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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A; Experimental source: strain DS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43; Mismatches
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A; Genome: plasmid
                                                                                                                                                                                             : || |::|
296 A-GVRLSDDVQRRIEDI 311
                                                                                                                                                      180 LNNLEFSDAELEAIDEI 196
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A; Residues: 1-336 <FAR>
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C; Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 18-Feb-2000
C;Accession: C6477
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-324 <STO>
A;Cross-references: GB:AE005174; NID:g12513275; PIDN:AAG54769.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable NAD(P)H-dependent xylose reductase yajo [imported] - Escherichia or C;Species: Escherichia coli C;Species: Escherichia E85538 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Steus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 PEGKTQLDQVRQISKIAEQIGATPSQLALAWTLKN-----PYVSTTILGASKPEQI--- 308
                                                                                                                                                                                                                                                                                                             144 PMEEVVRAFTQLIQDGKAFYWGTSEWS-AFEIEHAHHIATKYNLIAPVADQPQYNYLTRD 202
                                                                                                                                                                                                                                                                                                                                                                                                61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLNV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ----nnidmvrklndiaqergqslaqmalawvlreqgeygadtvtsaligassveqldns 176
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                                                                                                                                                                                                                              3 PLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL--LIHQPSYSIINRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 HFE-----KDLLPLQQIYGYGATVWSPLKSGILTGKYNDGIPEGSRLSTTFTSLAGQLQT
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                                                    Length 344;
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                                                                                                                                           Indels
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                                                                                                                                       75;
                                                        DB 2;
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                                                                                                Pred. No. 1.6e-10;
                                                                                                                                       37; Mismatches
                                                        Score 227.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 VENVKAVEFIDKLTPEILKKIDEI 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 LDSLNNLEFSD----AELEAIDEI 196
                                                    20.9%;
32.8%;
                                                                                                Best Local Similarity 32.88 Matches 67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross_references: GB:AE003888; GB:AE003849; NID:g9105187; PIDN:AAF83177.1; GSPDB:GN001
A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
Brisnipson, A.J.G.; Reinbach, E.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docena, C.; El-Dorry, H.F. Facincani, A.P.; Ferreira, A.J.S.
Bubmitted to Genbank, June 2000
A;Authors: Ferreira, W.C.A.; Ferro, J.A.; Frero, J.B.; Krieger, J.E.; Kuramee, E.E.; Laigr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramee, E.E.; Laigr A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Mench, C.F.M.; Margues, M.Y.; Martins, F.G.; Nunes, L.R.; Oliveira, M.A.; ac Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.B.; Aluthors: da Silva, A.C.R.; da Silva, A.C.; da Silva, A.C.; Savasak
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.
C; Genetics:
C; Genetics:
                                                                                       R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
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Gispectes: Schizosaccharomyces pombe
Gispectes: Schizosaccharomyces pombe
Gispectes: 30-bec-1999 #sequence_revision 03-bec-1999 #text_change 18-Feb-2000
Giscession: T41659
Riwood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
Riwood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
A.Rocession: T41659
A.Roc
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A83515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below A;Accession: F82815
A;Accession: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-387 <SIM>
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A;Map position: 3
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: XF0367
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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D.J.; May K.; Apoda

J.D.; Rose, Potamousis,

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probable oxidoreductase PA4434 [imported] - Pseudomonas aeruginosa (strain PAO1)
C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Sacession: B83093
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L., Lory, S.; Olon, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa A; Reference number: A82950; MUD: 20437337
A; Accession: B83093
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: Complete strain PAO1
C; Senetics: Complete strain PAO1
C; Schettics: Complete Strain PAO1
C; Data Strain PAD1
C; Data S
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C;Species: Solanum tubercsum (potato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 20-Jun-2000
C;Accession: T07394
R;Elge, S.
asubmitted to the EMBL Data Library, August 1997
A;Reference number: Z16006
A;Accession: T07394
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Resiques: 1-330 <ELG>A;Accession: EMBL: AJ000999; PIDN:CAA04451.1
A;Experimental source: CV. Desiree
C;Genetics:
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        240 WTEPPVRDEERLWNI-----UDTLLSVADGRGVSAAQVALAWLI------GRKAVTSIII 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 FE-----VGLAEIAIREQCGLLAYSPMAFGMLSGKYADGARPANARISLYSRFTR-YTN 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 345;
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Best Local Similarity 33.0%; Pred. No. 3.2e-09;
Matches 66; Conservative 33; Mismatches 85; Indels
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C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
C;Keywords: voltage-gated ion channel
                                                                                                                                                                                                                           319
                                                                                                                                      GASSVEQLDNSLDSLNNLEFSDAELEAIDEIS 197
                                                                                                                                                                                                | : | : : | : | : : | : | GRTEAQFKDNL-AAADLQLSAEERKRLDDVS
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321 V-DLRLDEEVLAGIDAIHRE 339
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A; Residues: 1-348 < BLATP>
A; Residues: 1-348 < BLATP>
A; Residues: 1-348 < BLATP>
A; Cross-references: GB:AE000148; GB:U00096; NID:g1786614; PIDN:AAC73522.1; PID:g1786621;
A; Experimental source: strain K-12, substrain MG1655
C; Genetics: A; Generics: A; 
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J. Bacteriol. 178, 3275-3284, 1996
A; Title: Ti plasmid-encoded genes responsible for catabolism of the crown gall opine man
by the plant tumor.
A; Reference number: 222872; MUID:96236046
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C;Species: Agrobacterium tumefaciens
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
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A; Residues: 1-354 <KIM>
A; Cross-references: EMBL:U19620; NID:g797330; PIDN:AAB07785.1; PID:g797336
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ-----GKSL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 SEGMLNVNNIDMVRKLNDIAQERGOSLAQMALAWVLREQGEYGADTVTSALIGASSVEQL 173
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                                                                                                                             Accession: C64771
Status: nucleic acid sequence not shown; translation not shown
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Science 277, 1453-1462, 1997
A,Title: The complete genome sequence of Escherichia coli K-12.
A,Reference number: A64720; MUID:97426617
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A;Genome: plasmid pTil5955
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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Similarity 32.5%; Pred. No. 2.3e-09;
59; Conservative 35; Mismatches 66;
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20.6%; Score 225; DB 2;
Best Local Similarity 31.9%; Pred. No. 2.6e-10;
Matches 60; Conservative 39; Mismatches 63;
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A; Status: preliminary; translated from GB/EMBL/DDBJ
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317 DELLNAVD 324
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Best Local Simi
Matches 69;
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Ouery Match
19.2%; Score 209; DB 2; Length 330;
Best Local Similarity 30.5%; Pred. No. 4.3e-09;
Matches 64; Conservative 40; Mismatches 70; Indels 36; Gaps
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 202; DB 2;
Pred. No. 3.3e-14;
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Two Prudential Plaza, Suite 4900
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23-FEB-1996
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5856155
                                                                                                     294 ENLGAIQVLPKMTSHVVNEIDNI 316
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TELECOMMUNICATION INFORMATION
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TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 3076
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TITLE OF INVENTION: COMI
TITLE OF INVENTION: COMI
TITLE OF INVENTION: COMI
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 64; Conserv
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STREET: TWC
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125 NTPMEEIVRAMTHVINQGMAMYWGTSRWSAMEIMEAYSVARQFNMIPPVCEQAEYHLFQR 184
                                                     60 WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQG--KSLSEGM 117
                                                                                      118 LNVNNIDMVRKLND---IAQERGQSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLD 174
                                                                                                                                                                                                    185 EKVE-----VQLPELYHKIGVGAMTWSPLACGIISGKYGNGVPESSRASLKCYQWLKERI 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Mismatches
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                                                                                                                                                                                                                                                                                                                                           294 ENLGAIQVLPKMTSHVVNEIDNI 316
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Patent No. 5856155
GENERAL INFORMATION:
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NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (312) 616-5600 (312) 616-5600 (312) 616-5700 (312) 616-5700 (312) 616-5700 (312) 616-5700 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-5600 (312) 616-
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I: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 329 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 31.0
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: L1, MIN
TITLE OF INVENTION: COMI
TITLE OF INVENTION: COMI
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-606-143-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60601
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COUNTRY:
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COMPOUNDS AND RELATED METHODS FOR ODDILATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH COMPOUNDS 9 185 EKVE----VQLPELFHKIGVGAMTWSPLACGIVSGKYDSGIPPYSRASLKGYQWLKDKI 239 1.3 LSEGMLNVNNIDMVRKLNDIAQERGOSLAQMALAWVLREQGEYGADTVTSALIGASSVEQ 172 1 DTPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEG-CPLLIHQPSYSIINR 59 22; Length 329; 60 WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRAS----Indels

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; Sequence 1, Application US/09215087; Patent No. 5981244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: B1111ngs, Lucy J.
REGIGSTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: Herewitl
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LIBRARY: BRAINOT14
; CLONE: 1596452
US-08-907-674-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: line
                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                              ZIP: 94304
                                                                                                                                                                                                              C
                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-09-215-087-1
                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 EEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGS--RASQGKSLSEGMLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 VNNIDMVRKLNDIAQERGOSLAQMALAWVLREQGEYGADTVTSALIGASSVEQLDNSLDS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMA-EEGCPLLIHQPSYSIINRWV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1114;
          Sequence 31. Application US/08576626A
Fatent No. 5998194
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Summers, R.G.
APPLICANT: Donadio, S.
APPLICANT: Staver, M.J.
TITLE OF INVENTION: POLXKETIDE-ASSOCIATED SUGAR
TITLE OF INVENTION: BIOSYNTHESIS GENES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.0%; Score 175; DB 2;
29.9%; Pred. No. 2.3e-10;
tive 38; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,626A
FILING DATE: 21-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 5857.US.O1
TELECOMMUNICATION:
TELEPHONE: (847) 938-3137
TELEFAX: (847) 938-2623
                                                                                                                                                                                                                            ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-907-674-1; Sequence 1, Application US/08907674; Patent No. 5919685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                  ZIP: 60064-300C
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CAMPHITER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No. 5998194e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1114 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                            CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE:
US-08-576-626A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQ
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61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ---GKSLSEGM 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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| ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 331;
APPLICANT: Shah, Purvi
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: Fast5EO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,674
FILING DATE: Herewith
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                                                                                                                                                                                                                                                                                                                                                    289 MSSLEQLEQNLAATEEGPLEPAVVDAFNQAWH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
CITY: Palo Alto
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118 LN-----VNNIDMVRKLNDIAQ-ERGQSLAQMALAWVLRE---QGEYGADTVTSALIG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ---GKSLSEGM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.9%; Score 162.5; DB 3; Length 331; 27.8%; Pred. No. 8e-10;
                                                                   APPLICANT: COLLEY, Neil C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, well C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                    SYSTEM: DOS
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Mismatches
                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 ASSVEQLDNSLDSLNNLEFSDAELEAIDEISH 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0362 US
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/391,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/907,674
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: B1111045, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-055
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08907674
Patent No. 5919685
                                                                                                                                                                                   3174 Porter Drive
                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 331 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LIBRARY: BRAINOT14
; CLONE: 1596452
US-09-391-959-1
                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Matches 59; Conserv
                                                                                                                                                                                     STREET: 3174 POI
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                    CA
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-08-907-674-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQ---GKSLSEGM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 VE-----TELFPCLRHFGLRFYAXNPLAGGLLTGKYKYEDKDGKQPVGRFFGNTWAEMY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 LN-----VNNIDMVRKLNDIAQ-ERGQSLAQMALAWVLRE---QGEYGADTVTSALIG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 RNRYWKEHHFEGIALVEKALQAAYGASAPSVJSAALRWMYHHSQLQGAHG----DAVILG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 331;
                                                                                                                                        HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
14.9%; Score 162.5; DB
Best Local Similarity 27.8%; Pred. No. 8e-10;
Matches 59; Conservative 34; Mismatches 5
APPLICANT: Shah, Purvi
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Noil C.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALD
NUMBER OF SEQUENCES: 3
CORRESPONDINCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/215,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11:|||::|| 289 MSSLEQLEQNLAATEEGPLEPAVVDAFNQAWH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 ASSVEQLDNSLDSLNNLEFSDAELEAIDEISH 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERNCE/DOCKET NUMBER: PF-0362 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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Sequence 1, Application US/09391959

Patent No. 6071704

GENERAL INFORMATION:

APPLICANT: Shah, Purvi

APPLICANT: Shah, Purvi

APPLICANT: Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/907,674
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: BRAINOT14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
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; CLONE: 1596452
US-09-215-087-1
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118 L-----OGEYGADTVTK-LNDIAQERGQSLAQMALAWVLRE---OGEYGADTVTSALIG 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Narl J.
APPLICANT: Corley, Narl J.
TITLE OF INVENTION: HUMAN AFLATOXIN B1 ALDEHYDE REDUCTASE
NUMBER OF SEQUENCES: 3
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 14.3%; Score 156.5; DB 2; Best Local Similarity 26.3%; Pred. No. 3.6e-09; Matches 57; Conservative 37; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 ASSVEQLDNSLDSLNNLEFSDAELEAIDE----ISHD 199
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                                                                                                                                                                                                                         FastSEQ for Windows Version 2.0
3: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,087
FILING DATE:
                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/907,674
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 3, Application US/09391959
; Patent No. 6071704
; GENERAL INFORMATION:
                                                                                        COUNTRI.

ZIP: 94304
COMPUTER READABLE FORM:
MEDUUM TYPE: Diskette
"""TIMPR: IBM COMPATIBLE
""" DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: ELBOTH: 327 amino acids TYPE: amino acid STRANDENNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenBank
                                                   Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LIBRARY: GenB
; CLONE: 433611
US-09-215-087-3
               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-391-959-3
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                                                   CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 L-----NVNNIDMVRK-LNDIAQERGQSLAQMALAWVLRE---QGEYGADTVTSALIG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 MDRYWKEEHFNGIALVEKALKTTYGPTAPSMISAAVRWMYHHSQLKGTQG----DAVILG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.3%; Score 156.5; DB 2; Length 327; 26.3%; Pred. No. 3.6e-09; Live 37; Mismatches 94; Indels 29
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Patent No. 5981244
CENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Cocley, Nail C.
TITLE OF INVENTION: UNAN AFLATOXIN BI ALDEHYDE REDUCTASE
NUMBER OF SEQUENCES: 3
                                                                                                                                                                      COMPUTE READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,674
FILING DATE: Herewith
CLASSIFTCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF-0362 US
                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/COCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 26.33
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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; CLONE: 433611
US-08-907-674-3
                                                                                                                                       USA
                                                                                                                                                         94304
                                                ADDRESSEE:
                                                                                                                 STATE: CA
                                                                                                                                       COUNTRY:
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TYPE: Amino Acid
STRANDEDNESS: Sin
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                                        Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: L. MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                           48864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LIBRARY:
US-09-166-412-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
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US-09-166-412-2
                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 MDRYWKEEHFNGIALVEKALKTTYGPTAPSMISAAVRWMYHHSQLKGTQG----DAVILG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 TPLEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPL-LIHQPSYSIINRW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 14.3%; Score 156.5; DB 3
Best Local Similarity 26.3%; Pred. No. 3.6e-09;
Matches 57; Conservative 37; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 ASSVEQLDNSLDSLNNLEFSDAELEAIDE----ISHD 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | | | | | : : | : : | : : | : : | : : | : : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
CUGFTWARE: FastSED for Windows Version 2.0
CUGFRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/391,959
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6-Phosphate Reductase
and Recombinants
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Patent No. 6133504
GENERAL INFORMATION:
APPLICANT: Wayne D. Loescher,
APPLICANT: John D. Everard
APPLICANT: Rebecca Grumet
TITLE OF INVENTION: DNA Encoding P
TITLE OF INVENTION: 6-Phosphate Re;
TITLE OF INVENTION: And Recombinat
TITLE OF INVENTION: Produced There
                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/907,674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY-AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEFAX: 415-845-4166
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2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 433611
                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                 COMPUTER READABLE FORM:
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Palo Alto
                                                                      USA
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STREET: 21
                                                                  COUNTRY:
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229 D-DPVLNDVAKKYGKSVAQICLRW------GIQRKTAVIPKSSKIQRLKENLEVL-FF 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LEETMYALRDIVASGKALYVGISSYGPELTAEAAEFMAEEGCPLLIHQPSYSIINRWVEE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.9%; Score 107.5; DB 4; Length 310; 20.8%; Pred. No. 0.00091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 PYFORDSLVKFCMKHGVLPTAHTPLG-GAAANKDMFG----
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6-Phosphate Reductase
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                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ian C. McLeod
REGISTATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MGU 4.1-275
TELECOMMUNICATION INFORMATION:
TELEFENNE: (517) 347-4100
TELEFAX: (517) 347-4103
INFORMATION FOR SEQ ID NO: 4:
                                                                                              OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: (version 3.3)
SOFTWARE: Wordperfect 5.1
SOFTWARE: APPLICATION DATA:
APPLICATION NUMBER: US/09/166,412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 kb storage
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/731,320
FILING DATE: October 15, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09166412
Patent No. 6133504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
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APPLICANT: John D. Everard
APPLICANT: Rebecca Grumet
TITLE OF INVENTION: DNA Encod
TITLE OF INVENTION: 6-Phospha
                                                                             COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single
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APPLICANT: MIKIKO SUGA, Masakazu SUGIMOTO, Tsuyoshi OSUMI, Tsuyoshi NAKAMATSU, TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY FERMENTATION FILE REFERENCE: 09813 CURRENT APPLICATION NUMBER: US/09/222,817 CURRENT FILING DATE: 1998-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 WVEEPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQGKSLSEGMLN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 YLQQP-----RLIEFAQSRGIAVTAYSSF------GPQSFVELNQGRALNTSPLF 236
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                                                                                                    APPLICANT: Hahn-Hagerdal, Barbei
APPLICANT: Waldfridsson, Mats
APPLICANT: Airaksinen, Ulla
TITLE OF INVENTION: XYLOSE UTILIZATION BY RECOMBINANT YEASTS
UNMBER OF SEQUENCE: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.7%; Score 106; DB 2; Length 318; 24.2%; Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/336,198C
FILING DATE: 03-N0V-1994
                                                                                                                                                                                                                                             ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 N. Washington St. CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/09222817; Patent No. 6037154; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8050
                           Hallborn, Johan
Penttila, Merja
                                                                                             Keranen, Sirkka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 703-205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 318 amino acids
amino acid
                                                                     Ojamo, Heikki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 24.2
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-198C-3
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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288 -LDEQDFADIAKLD 300
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                                                                                                                                                                                                                                                                                                                   Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                ADDRESSEE:
STREET: 301
                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 DPVLKKLSD---KHNKSPAQIVLRW------GVQRNTIVIPKSSKTKRLEENI-NIFD 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.7%; Score 106; DB 4; Length 309; 20.4%; Pred. No. 0.0013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/731,320
FILING DATE: October 15, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MGV 4.1-275
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECENX: (517) 347-4103
INFORMATION FOR SEQ ID NO: 2:
                         Produced Therefrom
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 kb storage
COMPUTER: 18M Compatible
OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: (version 3.3)
SOSTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,412
TITLE OF INVENTION: and Recombinants
TITLE OF INVENTION: Produced Therefr.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                              ...urgSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos STATE: Michinar
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Matches 42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Amino Acid
STRANDEDNESS: Single
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                                                                                                                                                       STATE: Michigan
COUNTRY: USA
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                                                                                                                                                                                                                                                                            Length 530;
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APPLICANT: MIXIKO SUGA, MASAKAZU SUGIMOTO, TSUYOSHI
TITLE OF INVENTION: METHOD OF PRODUCING L-SERINE BY
FILE REFERENCE: OP813
CURRENT APPLICATION NUMBER: US/09/222,817
CURRENT FILING DATE: 1998-12-30
EARLIER FILING DATE: 1998-01-12
EARLIER FILING DATE: 1998-01-12
EARLIER FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                          Query Match 8.8%; Score 95.5; DB 3; 3
Best Local Similarity 23.6%; Pred. No. 0.047;
Matches 59; Conservative 30; Mismatches 106;
EARLIER APPLICATION NUMBER: JP 10-3751
EARLIER PILING DATE: 1998-01-12
EARLIER APPLICATION NUMBER: JP 10-353521
EARLIER FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 12
LENGTH: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/09222817 Patent No. 6037154
                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Brevibacterium flavum
US-09-222-817-12
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; ORGANISM: Brevibacterium flavum
US-09-222-817-14
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SEQ ID NO 14
LENGTH: 530
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model Run on: September 13, 2001, 17:51:44 ; Search time 34.57 Seconds (without alignments) For in the core: 1460 Sequence: 1460 Sequence: 1460 Sequence: 1460 Sequence: 1460 Sequence: 1460 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 412676 seqs, 60623988 residues Total number of hits satisfying chosen parameters: 412676 Maximum DB seq length: 0 Maximum Match 1000 Post-processing: Minimum Match 1000 Listing first 45 summaries Database: A_Geneseq_0601:* 1: /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:* 3: /SIDSB/gcgdata/geneseqp/AA1981.DAT:* 4: /SIDSB/gcgdata/geneseqp/AA1981.DAT:* 5: /SIDSB/gcgdata/geneseqp/AA1981.DAT:* 6: /SIDSB/gcgdata/geneseqg/geneseqp/AA1981.DAT:* 6: /SIDSB/gcgdata/geneseqg/geneseqg/geneseqp/AA1981.DAT:* 6: /SIDSB/gcgdata/geneseqg/geneseqg/geneseqp/AA1981.DAT:* 6: /SIDSB/gcgdata/geneseqg/geneseqg/geneseqp/AA1981.DAT:* 7: /SIDSB/gcgdata/geneseqg/geneseqg/geneseqg/geneseqg/AA1981.DAT:* 8: /SIDSB/gcgdata/geneseqggenesegg/gene	7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:* 8: /SIDS8/gcgdata/geneseqfyAA1986.DAT:* 9: /SIDS8/gcgdata/geneseqg/geneseqpyAA1987.DAT:* 10: /SIDS8/gcgdata/geneseqg/geneseqpyAA1989.DAT:* 11: /SIDS8/gcgdata/geneseqg/geneseqpyAA1999.DAT:* 12: /SIDS8/gcgdata/geneseqg/geneseqpyAA1991.DAT:* 13: /SIDS8/gcgdata/geneseqg/geneseqpyAA1991.DAT:* 14: /SIDS8/gcgdata/geneseqg/geneseqpyAA1991.DAT:* 15: /SIDS8/gcgdata/geneseqg/geneseqpyAA1991.DAT:* 16: /SIDS8/gcgdata/geneseqg/geneseqpyAA1991.DAT:* 17: /SIDS8/gcgdata/geneseqg/geneseqpyAA1995.DAT:* 18: /SIDS8/gcgdata/geneseqg/geneseqpyAA1995.DAT:* 19: /SIDS8/gcgdata/geneseqg/geneseqpyAA1999.DAT:* 20: /SIDS8/gcgdata/geneseqg/geneseqpyAA1999.DAT:* 21: /SIDS8/gcgdata/geneseqg/geneseqpyAA1999.DAT:* 22: /SIDS8/gcgdata/geneseqg/geneseqpyAA1999.DAT:* 23: /SIDS8/gcgdata/geneseqg/geneseqpyAA1999.DAT:* 24: /SIDS8/gcgdata/geneseqg/geneseqpyAA1999.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	C. glutamicum Lys	Corynebacterium ql	ORFL16 protein inv	SnpR activator pro	Amino acid sequenc	Neisseria meningit	Neisseria meningit	Protein encoded by	Amino acid sequenc	S. venezuelae macr	Narbonolide syntha	
	ID	AAW37714	AAB79658	AAY39317	AAW36129	AAB30494	AAY74592	AAY74593	AAY29277	AAB18640	AAY77195	AAY67204	
	DB :	18	22	20	19	21	21	21	20	21	21	21	
	Query Match Length DB	290	290	278	311	311	299	299	344	1346	1346	1346	
#P	Query Match	100.0	100.0	8.1	7.2	7.2	7.0	7.0	6.9	6.8	6.8	6.8	
	Score	1460	1460	118.5	105	105	102.5	101.5	100.5	99.5	99.2	99.5	
	Result No.	-	7	٣	4	S	9	7	80	σ	10	11	

S. venezuelae pik Neisseria gonorrhe A. mediterranel ri Truncated irge. v Streptomyces antib KsqMq loading di S. antibioticus 8, E. coli bioSl prot Plasmid pHSl bioSl Plasmid pHSl bioSl DE19731274 Seq ID DE19731274 Seq ID DE19731274 Seq ID E. coli biotin ORF C. coli biotin ORF C. coli biotin ORF C. coli biotin ORF S. venezuelae pik Bud promoter trans S. clavuligerus OR Sorangium cellulos Requiatory protein	Boyine p57 protein Cellulose synthase Neisseria meningit Human ORFX ORF2255 Amino acid sequenc S. venezuelae macr S. venezuelae pik Narbonolide syntha Protein encoded by S. antibioticus 8 Cephalosporin anti Phosphoenolpyruvat A. mediterranei ri SpnB a polyketide Tylactone synthase
AAY77180 AAY74591 AAW552846 AAR55584 AAX77292 AAX77292 AAX33264 AAX933264 AAX932936 AAW92936 AAW92936 AAW92936 AAW92936 AAW92936 AAW92936 AAW92936 AAW92936 AAW92936 AAX7865	AARS93474 AAR9342451 AAR92451 AAB42491 AAB42491 AAR77193 AAR67202 AAR66467 AAR96949 AAR96949 AAR96949 AAR92848
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ALIGNMENTS

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AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleosides, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
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                               99DE-1031434.
99DE-1031435.
99DE-1031443.
99DE-1031453.
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08-JUL-1999;
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                                          This sequence is the LysG protein product, a lysine export regulator. LysG and LysE encode a lysine transport regulatory protein and an export protein, respectively. Microbial production of amino acids (A) is improved by increasing the export-carrier activity and/or the export gene expression in a microorganism that produces (A). The method is specifically used to increase production of lysine, used as an animal feed additive. Other (A) are variously useful as plarmaceuticals, condiments and intermediates for fine chemicals. This method increases the amount of (A) secreted into the culture medium. Export of (A) has been found to depend on a single gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
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Best Local Similarity 100.0%; Score 1460; DB 18; Length 290;
Best Local Similarity 100.0%; Pred. No. 3.2e-150;
Matches 290; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum MP protein sequence SEQ ID NO:50.
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                Disclosure; Page 6; 16pp; German.
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99DE-1030476.
99US-0142101.
99DE-1031415.
99DE-1031419.
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01-JUL-1999;
02-JUL-1999;
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08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                               Spinosyn biosynthetic enzyme; open reading frame; ORF; insecticidal microlides; arachnid; nematode; insect; polyketide; polyketide synthase; PKS; extender module; initiator module; acyl transferase domain; AT; acyl carrier protein; ACP; beta-ketosynthase domain; KS; KR; Redoydratase domain; BH; enoyl reductase domain; ER; beta-ketoreductase; insecticide; transcriptional control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New spinosyn biosynthetic genes from Saccharopolyspora spinósa, useful for production of insecticidal spinosyn compounds
                                                                                                                   EVLVQAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTL 120
                                                                                                                                RLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLD 180
                                                                                                                                                                       WAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQA 240
                                                                                                                                                                                                              Gaps
                                                                             1 MNPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAG 60
                                                                                        ;
0
                                       Length 290;
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                                                          Indels
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                                      100.0%; Score 1460; DB 22;
ilarity 100.0%; Pred. No. 3.2e-150;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                              ORFL16 protein involved in spinosyn biosynthesis.
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Waldron C;
                                                                                                                                                                                                                                                                                                                 AAY39317 standard; Protein; 278 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DOWC ) DOW AGROSCIENCES LLC
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Treadway PJ, Turner JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-551414/46.
                                               Similarity
         AA;
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         290
                                      Query Match
Best Local Simil
Matches 290; (
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         Sequence
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insects. Blosynthesis of spinosyns occurs via stepwise condensation and insects. Blosynthesis of spinosyns occurs via stepwise condensation and insects. Blosynthesis of spinosyns occurs via stepwise condensation and additication of carboxylic acid precursors generating a linear polyketide which is modified further. The DNA sequence contains a central region of approximately 55kb which has homology to the DNA encoding the polyketide synthases (FKS) of known macrolide producers. The spinosyn PKS DNA region consists of 50 Known macrolide producers. The spinosyn PKS DNA region consists of 50 Known mitiator module, spnA, and several carted modules spnB-spnE. The products of the genes present in the region upstream of the PKS genes have been assigned names spnB-spnS region upstream of the PKS genes have been assigned names spnB-spnS region upstream of spnS, producting polypeptides and are responsible for different modifications in spinosyn blosynthesis. There are also two ORFS ORFLIS and ORFLIS free producing polypeptides AAY39318 '139319' it is suggested that the ORFLIS producing polypeptides AAY39318 '139319' it is suggested that the ORFLIS producing polypeptides AAY39318 '139319' it is suggested that the ORFLIS producing polypeptides AAY39318 '139319' it is suggested that the ORFLIS producing polypeptides AAY39318 '139319' it is suggested that the ORFLIS producing polypeptides AAY39318 '139319' it is suggested that the ORFLIS producing polypeptides AAY39318 '139319' it is suggested that the ORFLIS producing polypeptides AAY39318 '139319' it is suggested that the ORFLIS producing polypeptides and series are useful to improve yields of spinosyns, and for creating new spinosyns e.g. by mutagenesis, or interruption of steps in spinosyn biosynthesis. The modified spinosyns may be a new insect control agent or serve as substrates for further chemical modification and the creation of new semi-synthesic spinosyns. The genes are also useful to isolate similar sequences from S. spinosa or other species by
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/note= "alpha-helix-beta-turn-alpha helix
DNA-binding domain"
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rain C5; SnpA; S. venezuelae; alpha-amylase; tumour growth; angiogenesis.

s sp. strain C5; cancer; tumour g

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Amino acid sequence of SnpR encoded by plasmid pANT1201
                                                                 Streptomyces sp.
                                                                                     WO200060945-A1.
                                  Streptomyces
                                           endostatin;
                                                                                                          19-OCT-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQP-AKATEAGEVLV 64
                                                                                                                                                                                                                                                 activator gene. The single activator gene is incorporated in novel plasmid pANT195 (see AAV01451) that also includes the snpk-activated snph promoter and a modified doxA gene (see AAV01447) of Streptomyces sp. strain C5. The doxA gene codes for daunomycin C-14 hydroxylase (see AAW36128), an enzyme capable of converting daunomycin to the anticancer agent doxcrubicin. Host cells, especially Streptomyces host cells, transformed with pANT195 daunomycin or for the hydroxylation and oxidation of other
                                                                                                                                                                        Producing doxorubicin from daunomycin by daunomycin C14 hydroxylase also hydroxylation and oxidation of other anthracycline(s) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 DWAAMPVLRFGPKDVLQDRDLDGRVDGPVGR------RRVSIVPSAEGFGEAIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GLGWGLL--PETQAAPMLKAGEVILLDE--IPIDTPMYWQRWRLESRSLARLTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 vlraegldsrilhgdyhsaaylvatgevvtvvqptspsraetavrrlhgdplgvrlllaa
                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                         This protein is the encoded product of the Streptomyces snpR
                                                                                                                                                                                                                                                                                                                                                                                                        Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                       7.2%; Score 105; DB 19; 121.2%; Pred. No. 0.0052; ative 50; Mismatches 129;
                                                                                                                    Strohl WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB30494 standard; Protein; 311 AA.
                                                                                                                                                                                                                    Disclosure; Fig 6; 59pp; English.
                                                                                             (OHIS ) UNIV OHIO STATE. RES
                                                    97WO-US08690
                                                                         96US-0653650
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 21.29
Matches 66; Conservative
                                                                                                                   Dickens ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 VVDAAIEGLRP 290
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                                                                                                                                         WPI; 1998-018495/02
                                                                                                                                                                                                                                                                                                                                                                        311 AA;
                                                                                                                                                    N-PSDB; AAV01451
                                                                                                                                                                                               the same enzyme
                                                                                                                                                                                                                                                                                                                                                     anthracyclines.
         WO9744439-A2
                                                    22-MAY-1997;
                                                                         24-MAY-1996;
                                                                                                                   DeSanti CL,
                              27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                         Sequence
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The present sequence is encoded by a fragment of pANT1201. This plasmid was used as a source of snpk, snph promoter, and multiple cloning site. The specification describes a method for the production of soluble, recombinant human endostatin in Streptomyces. Leader sequences of streptomyces sp. strain C5 Snph and S. venezuelae alpha-amylase proteins are linked to the N-terminal of endostatin. This ensures that endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. The method is used for preparing soluble recombinant human, murine or primate endostatin, which is useful in the treatment of cancer, inhibition of tumour growth, inhibition of angiogenesis, isolation of encounted compounds in assays. The endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. Streptomycetes are amenable for cultivation in large fermentations allowing for large quantities of soluble endostatin to be produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 QAARKMVL----LQAETKAQLSGRLAEIPLTIAINAD-SLSTWFPPVFNEVASWGGATLT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 LRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQP-AKATEAGEVLV 64
                                                                                                                                                                                                                                                                                                                                                                                         Preparation of soluble recombinant endostatin involves transforming Streptomycete host with expression vector comprising nucleotide sequence encoding endostatin operably linked to linker and leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   srarplvaelcslvseara---aavadaslrvgstasralagw----lrrlrhwqeptlh
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166 qfvclp------adhpaaeatsyasptwpttrwmidptvdgewnavrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DWAAMPVLRFGPKDVLQDRDLDGRVDGPVGR------RRVSIVPSAEGFGEAIRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 105; DB 21;
Pred. No. 0.0052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 9A-B; 57pp; English.
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21.2%;
12-APR-2000; 2000WO-US09747.
                                                                      99US-0129084
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                                                                                                                                                                                                                      Desanti CL, Strohl WR;
                                                                                                                                            (MERI ) MERCK & CO INC.
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N-PSDB; AAC62024.
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Best Local Similarity
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                                                                      13-APR-1999;
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06-MAR-2001 (first entry)

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Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
                                                                                                            -----VASWGGATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRH 161
                                                                                                                           2 NPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAG
                                                                                   agyfrragrilgemaaaetemla-vheipggvl----svdsampmvlhllaplaakfner
                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis ORF 158 protein sequence SEQ ID NO:660.
                                                             61 EVLVQAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hickey E,
Ratti G,
                                                                                                                                                                                                                                                   AAY74593 standard; Protein; 299 AA.
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Rappuoli R,
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98US-0098994
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99US-0121528
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Tettelin H, Venter JC;
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N-PSDB; AAZ53355.
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                                                                                                                                                             162 LAIATP 167
                                                                                                                                                                                       165 rviasp 170
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02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
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25-FEB-1999
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                                                                                                                                                                                                                                                               AAE53015 to AAE54536, AAE54577 to AAE54615, and AAY74253 to AAY5941 and polypeptides. AAE54576 and AAE54616 to AAE5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                             Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Masignani V, Mora M;
Scalato E, Scarselli M;
208 vlraegldsrilhgdyhsaaylvatgevvtvvqptspsraetavrrlhgdplgvrlllaa 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel Neisserial polypeptides predicted to be useful antigens for
                                                                                                                                                                                      Neisseria meningitidis ORF 158 protein sequence SEQ ID NO:658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 102.5; DB: 26.3%; Pred. No. 0.0092; ative 31; Mismatches 6
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Ratti G,
                                                                                                            AAY74592 standard; Protein; 299 AA.
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Rappuoli R,
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98US-0098994.
98US-0099062.
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98US-0103794
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99US-0121528
                                                                                                                                                              (first entry)
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Tettelin H, Venter JC;
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268 rtdtelegvyp 278
                       280 VVDAAIEGLRP 290
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Best Local Similarity
Matches 49; Conserv
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09-OCT-1998;
25-FEB-1999;
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represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ5453 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as manufacture of medicaments for treating or preventing in the neisserial bacteria (e.g. meningitis and septicaemia), to detect the
Masignani V, Mora M;
Scalato E, Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
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Gaps

39;

67; Indels

Conservative

9

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WPI; 2000-610844/58
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06-MAY-1998
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                                            Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding bylypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a P. aeruginosa infection.
presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                       EVLVQAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPV-----FNE- 109
                                                                                                                                                                                    119 yphirlslvssegyinlierkvdia----lragel-----ddsglrarhlfdsrf 164
                                                                                                                                                                                                                 -----VASWGGATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRH 161
                                                                                                           Gaps
                                                                                                                               9
                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a Pseudomonas aeruginosa polypeptide
                                                                                                                              2 NPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAG
                                                                                                                                           39;
                                                                                    DB 21; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mahajan-Miklos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virulence factors useful in developing disease treatments
                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection.
                                                                                                         67;
                                                                                    7.0%; Score 101.5; DB
26.9%; Pred. No. 0.012;
ilve 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goodman HM,
                                                                                                                                                                                                                                                                                                                                  AAY29277 standard; Protein; 344 AA.
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                                                                                                         Conservative
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Tan M, 1
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Best Local Similarity
Matches 50; Conserv
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                                                     299 AA;
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Narbonolide synthase; polyketide synthase gene; narbonolide polyketide; antibiotic; C12-hydroxyalse; picK; desosamine biosynthesis; desosaminyl transferase enzyme; ketolide; beta-glucosidase enzyme;
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                                                                                                                                                                                                                                                                                                                                                                                                                               TLTLRLEDEAHTLSLLRR--GDVLGAVTREANPVAGCEVVE------LGTMRHL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 vvahpghplcmaslhsiaslanyrqislgsrsgghsmll-----rpvs-dkvlfve 219
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                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                  6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEAGEVLV 64
in some instances assumptions were made as to the identity of the residue; it is therefore possible that the sequence given below is not entirely correct.
                                                                                                                                                                                                                                                                              pymrsllnyg----qlig-----diafnlnkgprnlrvlldtaippsfcd-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 AIATPS----LRDAYMVDGKLDWAAMPV-LRFGPKDVLQDRDLDGRVDGPVGRRRVSIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILLDEI----PIDTPMY-WQRWRLES-R
                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of narbonolide synthase subunit 4 (PICAIV).
                                                                                                                                                         Length 344;
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                                                                                                                                                              DB 20;
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; Pred. No. 0.019;
47; Mismatches 128;
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99US-0134990.
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98US-0073538.
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70; Conservative
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                                                                                          344 AA;
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280 sfrrfles 287
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WO200000620-A2

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The present sequence represents a narbonolide synthase subunit 4

(PICAIV). The nucleotide sequence encoding it is used in the course of the invention. The specification describes a recombinant bank compound expressing recombinant polyketide synthase genes in host cells for the production of narbonolide, narbonolide derivatives and polyketides that are useful as antibiotics and as intermediates in the synthesis of compounds with pharmaceutical value. The DNA compounds may also encode a C12-hydroxyalse (picK), desosamine biosynthesis and desosaminyl cransferase enzymes (useful for conversion of ketolides to antibiotics), and the beta-glucosidase enzyme (involved in picromycin biosynthesis). These compounds are also useful for increasing the antibiotic activity of a compound relative to the unhydroxylated compound. The recombinant of a compound relative to the unhydroxylated compound. The recombinant of the narbonolide polyketide synthase. These would be valuable for the narbonolide polyketide synthase. These would be valuable for creating novel ketolide analogs for pharmaceutical applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
New recombinant pick hydroxylase gene of Streptomyces venezuelae useful for converting ketolides to antibiotics and as antibiotics and intermediates in the synthesis of compounds with pharmaceutical value
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 EGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAG-----EVLVQAAR----- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           801 wyrnlrhrvgfapavetlatdegfthfievsahpvltmtlpdkvtglatlrred-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.8%; Score 99.5; DB 21;
20.9%; Pred. No. 0.18;
iive 35; Mismatches 107;
                                                                                                                                     Disclosure; Columns 13-14; 117pp; English.
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Matches 67; Conserv
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a g ŏ δλ Pp ò ŏ Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; blopolymer; antiblorite; chemcherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent. S. venezuelae macrolide biosynthetic enzyme PikAIV, SEQ ID NO:37. AAY77195 standard; Protein; 1346 AA. 954 qaasvlrcdspeevpvdrpl 973 05-JUN-2000 (first entry) AAY77195; 10

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Streptomyces venezuelae ATCC15439.

The INVELLOR ITERATES to an ISOLATER and pullicating and comprising a desocamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryc gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster are combination of these compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the decomposition of biologically active macrolides. The macrolide biosynthetic gene clusters are useful for the compounds are useful for synthesis of methymycin, pikromycin, pikromycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide production of biologically active macrolides. The macrolide biosynthetic cyprotesis may be useful to prepare novel antibiotics and polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkancate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biologically active agents, such as chemotherapeutics.

C biomedical applications, to engineer PHA monomer synthases or to prepare to biologically active agents, such as chemotherapeutics.

C biomedically active agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., as viral parasitic pathogens, or as crop protection agents (e.g., as viral parasitic pathogens, or as crop protection agents (e.g., as viral parasitic pathogens, or as crop protection agents (e.g., as viral parasitic pathogens, or as crop protection agents (e.g., as viral parasitic pathogens, or as crop protection agents (e.g., as traptomyces venezuelae ATCC 15439, which are encoded by sequences e .g. purified nucleic acid segment 69 -KMVLLQ-------AETKAQLSGRLAEIPLTIAINADSLSTW------745 ariipvdyashsahvetieneladvlaglspqtpqvpffstle----gtwitepaldggy -----FPPVFNEVASWGGAT------LTLRLEDEAHTLSLLRRGDVLGAVT 801 wyrn1rhrvgfapavet1atdegfthfievsahpv1tmt1pdkvtg1at1rred-----------ggghrl---ttslaeawanglaldwasllpatgalspavpdlptya Desosamine and macrolide biosynthetic gene clusters, useful for, 6.8%; Score 99.5; DB 21; Length 1346; 20.9%; Pred. No. 0.18; iive 35; Mismatches 107; Indels 111; 19 EGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAG-----EVLVQAAR--The invention relates to an isolated and synthesis of methymycin and pikromycin Claim 19; Page 424-428; 438pp; English. Zhao L; Liu H, Xue Y, 99WO-US14398 98US-0105537 Local Similarity 20.9 nes 67; Conservative (MINU) UNIV MINNESOTA WPI; 2000-160679/14. 1346 AA; N-PSDB; AA287300 AAZ87295-287302 Sherman DH, 25-JUN-1999; 26-JUN-1998; 06-JAN-2000. Sequence Query Match 103 855 Matches QQ

Length 1346;

DB 21;

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Query Match
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   953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Narbonolide polyketide synthase; PKS; narbonolide synthase subunit 4; PICAIV; antibiotic production; narbomycin; picromycin; ketolide.
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898 fqhrsywispagp-geapahtasgreavaet---glawgpgaedldeegrrsavlamvmr
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                                                                                                                                                                                                                                                                         AAY67204 standard; protein; 1346 AA.
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                                                         245 KAGEVILLD---EIPIDTPM
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                                                                                                Ashley G, Betlach MC,
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22-SEP-1998;
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                                                                                            :| ::|::| | ||::| | : : | | : ||68 kggmislalseeatrgrien|h---glsiaavngptatvvsgdptqiqelaqaceadgir 744
                                                                                                                                                                                                                                                                                                                                                                                                    898 fqhrsywispagp-geapahtasgreavaet---glawgpgaedldeegrrsavlamvmr 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated and purified nucleic acid segmen comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide
                                                                       ---EVLVQAAR---- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase;
blopolymer; antiblotic; chemotherapeutic; immunosuppressant; asthma,
chronic obstructive pulmonary disease; respiratory inflammation;
hypercholesterolaemia; crop protection agent.
                                                                                                                                                                    195 LQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPE-----TQAAPML
                                                                                                                                                                                                                    103 ------FPPVFNEVASWGGAT------LTLRLEDEAHTLSLLRRGDVLGAVT
                                                                                                                                                                                                                                        143 REANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM-----PVLRFGPKDV
                                                                                                                                                                                                                                                                                                                          ------ggqhrl---ttslaeawanglaldwasllpatgalspavpdlptya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. venezuelae pik gene cluster-encoded protein, SEQ ID NO:6.
                                                                                                                                              -----AETKAQLSGRLAEIPLTIAINADSLSTW
                                   107;
                                                                       19 EGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAG-
                                   35; Mismatches
 Score 99.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 19; Page 315-353; 438pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY77180 standard; Protein; 12199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces venezuelae ATCC15439
6.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        245 KAGEVILLD---EIPIDTPM 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xue Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US14398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-160679/14.
                  Best Local Similarity
                                                                                                                                              69 -KMVLLQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ87285
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                                   67;
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11-NOV-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, pikromycin, neomethymycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be moromers. The compounds produced by the recombinant host cells are useful so biomedia produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to as biopolymers produced by the recombinant host cells are useful as chemotherapeutics, immunosuppressants, agents to treat astima, chronic obstructive pulmonary disease as well as other diseases involving
                                                                                                                                                                                                                       respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of encoded by the macrolide biosynthetic gene cluster (pik) from Streptomyces venezuelae ATCC 15439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11427 ....----ggqhrl---ttslaeawanglaldwasllpatgalspavpdlptya 11469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11260 kggmislalseeatrgrien1h---glsiaavngptatvvsgdptgigelagaceadgir 11316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 ------FPPVFNEVASWGGAT------LTLRLEDEAHTLSLLRRGDVLGAVT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 REANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM------PVLRFGPKDV 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 LQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPE-----TQAAPML
                                                                                                                                                                                                                                                                                                                                                                                                                         6.8%; Score 99.5; DB 21; Length 12199; 20.9%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AETKAQLSGRLAEIPLTIAINADSLSTW----
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4.6;
35; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY74591 standard; Protein; 303 AA.
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Matches 67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       12199 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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WO9957280-A2

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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAX75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54574 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves may also be used as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
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                                                                                                                                                                                                                                                                                                                                           Mora M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel Neisserial polypeptides predicted to be useful antigens for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.7%; Score 98; DB 21; Length 303; 27.6%; Pred. No. 0.029; Live 28; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                        Masignani V,
Scalato E, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 yphirlslvssegyinlierkvdia----lragel 149
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Ratti G,
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                                                                                                                                                                                                                                                                                                                                        Grandi G,
Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 452; 1453pp; English.
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                                                                                         98US-0098994.
98US-0099062.
98US-0103749.
99WO-US09346
                                                                       98US-0094869
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98US-0103796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 27.6%
watches 43; Conservative
                                                                                                                                                                                                                                                                                       (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                               Petersen J, Pizza M, I
Tettelin H, Venter JC;
                                                                                                                                                                                                                                                                                                                                     Galeotti C,
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-062150/05.
                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAZ53353.
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30-APR-1999;
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09-0CT-1998;
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                                                                                              02-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW52846;
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XXEX
XXEX
XXEX
XXEX
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Cholera vaccine comprising live attenuated Vibrio cholerae cells - contains mutations which inhibit expression of a functional irgA gene product, vaccine has reduced virulence, decreasing side
                                                                                                                                                                  Virulence factor; intestine; multi-valent vaccine.
AAR25588 standard; Protein; 298 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 13; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calderwood SB, Goldberg MB,
                                                                                                                                                                                                                                                                                                                                                                                                                    (GEHO ) GEN HOSPITAL CORP. (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-250077/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ26543.
                                                                                                                                                                                                       Vibrio cholerae.
                                                                                                                         Truncated irgB.
                                                                                08-JAN-1993
                                                                                                                                                                                                                                                                                                                                  18-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                             18-DEC-1990;
                                                                                                                                                                                                                                                  WO9211354-A
                                                                                                                                                                                                                                                                                           09-JUL-1992.
                                         AAR25588;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a Amycolatopsis mediterranel rifamycin synthesis gene cluster ORF B protein from the present invention. The DNA fragment comprises a DNA region involved directly or indirectly in the gene cluster responsible for rifamycin synthesis, including the adjacent DNA regions to the right and left which, by reason of their function in connection with rifamycin blosynthesis, qualify as constituents of this rifamycin gene cluster, and functional fragments, derivatives or constituents of these. The Amycolatopsis mediterranel rifamycin synthesis gene cluster DNA fragment can be used for producing rifamycin, rifamycin analogues or precursors. It can also be used for inactivating or modifying genes involved in ansamycin or rifamycin blosynthesis, The DNA can be used for constructing mutant rifamycin blosynthesis gene cluster has been partly or completely deleted. The DNA fragment can be used for assembling a library of polyketide.

Synthases, which can be used for assembling a library of polyketides. A hybridisation probe of the invention can be used for identifying DNA fragments involved in the biosynthesis of ansamycins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAHTLS----LLRRGDV-LGAVTRE------ANPVAGCEVVELGTMRHLAIATPSLRD 171
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                                                                                                                                                                                                                                                                                                                                                                                               Amycolatopsis mediterranei rifamycin synthesis gene cluster - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79;
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Best Local Similarity 23.7%; Pred. No. 3.4;
Matches 71; Conservative 45; Mismatches 104; Indels
polyketide synthase; actinomycete; ansamycin
                                                                                                                                                                                                                                                                                                                                                                                                                    to produce rifamycin and rifamycin analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 126-151; 205pp; English.
                                                                                                                                                                  97WO-EP04495
                                                                                                                                                                                                       96EP-0810551
                                      Amycolatopsis mediterranei
                                                                                                                                                                                                                                                                                         Schupp T,
                                                                                                                                                                                                                                                                                                                              WPI; 1998-169172/15.
N-PSDB; AAV21187.
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                                                                             WO9807868-A1
                                                                                                                                                              18-AUG-1997;
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                                                                                                                       26-FEB-1998
                                                                                                                                                                                                                                                                                         Engel N,
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Mekalanos JJ;

91WO-US09592. 90US-0629102

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11;
The functional irgB gene encodes a protein which acts as a positive regulator of irgA. IrgA functions as a V cholerae virulence factor. The sequence given shows a truncated irgB. This truncation of the sequence inhibts expression of a functional irgA gene product in the cell. This sequence can be used to transform V cholerae calls which can then be used to induce immunity to cholera in a mammal. These transformed cells can colonize the intestines of inoculated animals and may be combined with vaccines targeted at other illnesses to make a single multi-valent vaccine. The transformed cells have reduced virulence such that the inoculated animal is less likely to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSL---RDAYMVDGKL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 KMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRL----- 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 sltaaakaleqpkstisrilaqleedlgqsilmrqgnrltltkagevfavyseqllelan 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 SFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEAGEV-----LVQAAR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 sdevfepdli-----iwiehaapmgyrkerlgywryatyaspkylahrd----
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 93.5; DB 13; Length 298;
Pred, No. 0.087;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4%; Sco. 23.0%; Pred. No. v... 33; Mismatches
                                                                                                                                                                                                                                                                                                           side effects such as diahhorea and fever
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224 amgadaiakgrgigllp 240
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nes 59; Conserv
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4088 agivdggy-wy-----gfgpavaelvr 4115

RESULT 15 P AAR25588

231 -GWGLLPETQAAPMLKAGEVILLDEIPIDTPMYWQRWRLESRSLARLTDAVVDAAIEGL 288

172 AYMVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGL- 230

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Search completed: September 13, 2001, 17:51:47 Job time: 1118 sec



Sequence 8, Appli Sequence 2, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 7, Appli Sequence 1, Appli Sequence 11, Appli Sequence 23, Appli Sequence 23, Appli Sequence 2, Appli Sequence 11, Appli Sequence 2, Appli

Title: Perfect score:

Run on:

Scoring table: Sequence:

Searched:

Database

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Sequence 27, Application US/07952817

Sequence 27, Application US/07952817

Patent No. 5356796

CENERAL INFORMATION:
APPLICANT: Keller, John W.
TITLE OF INVENTION: A Repressor Protein and Gene for Regulating
TITLE OF INVENTION: A Repression of Polypeptides and Its Use in the Preparation of TITLE OF INVENTION: 2,2-Dialkylglycine Decarboxylase of Pseudomonas Cepacia NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 LKTLQALRNSGSLAAAAAVLHQTQSALSHQFSDLEQRLGFRLFVRKSQPLRFTPQGEVLL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVG-RVLVSRTQPAKATEAGEVLV
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tive 29; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILOW
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/07/952,817
FILING DATE: 19220928
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 202-408
TELEPRAM: 202-408-4400
TELEPRAM: 202-408-4400
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TELEFAT. 275 amino acids
US-08-804-227C-8

US-08-961-198-2

US-08-961-198-2

US-08-961-038-2

US-08-380-403A-5

US-08-380-403A-5

US-08-895-628-2

US-08-895-628-2

US-07-952-817-11

US-07-952-817-23

S210025-4

US-08-843-521-2

US-09-012-871-2

US-09-012-871-2

US-09-013-814-89

US-08-476-519-11

PCT-US95-09323-12

US-08-476-519-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIF: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 23.9%
Matches 69; Conservative
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(without alignments)
307.477 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                               1 MNPIQLDTLLSIIDEGSFEG......RSLARLTDAVVDAAIEGLRP 290
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Sequence 28,
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Sequence 10,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-952-817-27
US-09-036-987A-22
US-09-320-814-4
US-07-952-817-28
US-08-614-686A-1
US-08-614-686A-1
US-08-413-697-25
US-09-335-409-6
US-09-335-409-6
US-09-335-410-26
US-09-113-825-2
US-09-113-825-2
US-09-113-825-2
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US-08-804-227C-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-911-853-7
US-09-479-409-7
                                                                                                                                                                                                                                                                                                                                                                                                                                     197339 segs, 20590346 residues
                                                                                                                                                                       September 13, 2001, 17:52:10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM protein – protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Score

Result No.

136.5 118.5 99.5 96

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Gaps 64

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118 LTLRLEDEAHTLSLLR--RGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYWV 175
                                                                                                                60 GEVLVQAARKMY--LLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGAT 117
                                                                                                                                                                    176 DGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEG------FGEAIR 227
                                                                                                                                                                                                              172 ---HPLASEPHVRMADVSSLPDLPL-ARWPGPDG-----VYPDGPGVEVRNOTOLFOMIA 222
                                                                                                                                                                                                                                                        228 RGLGWGLLPETQAAPMLKA-GEVILLDEIPIDTPMYWQRWRLESRSLARL 276
                                                                                                                                                                                                                                                                                  223 IGRTTVVMPESSRVNLLEGLAAVPVLDAPDVTTVIAWPP-HSRSRALAGL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 60/087,080 EARLIER FILING DATE: 1998-05-28
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09320878A Patent No. 6117659 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-320-878-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ASHLEY, Gary APPLICANT: BETLACH, Melanie C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 300622002120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BETLACH, Mary C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver.
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US-09-320-878-4
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  --GG 115
                                                                                                                    126 VTFDPQPALQQGELDLVWTSDILPRSELHYSPWFDFEVRLVLAPDHPLASKTQITPEDLA 185
                                       67 QLANQ-VLPQISRALQACNEPQQTRLRIAIECHSCIQWLTPALENFRASWPQVEMDFTSG 125
                                                                                                                                                                    -----YELGTMRHL---AIATPSLRDA-----YMVDGKLDWAAMPVLRFGPK 192
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APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                          186 SETLLIYPVORSRLDVWRHFLQPAGISPLLKSVDNTLLLIQMVAARMGIAALPHW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 278;
                                                                                                                                                                                                                                                    193 DVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAA 241
                                                                                                                                                                                                                                                                              Indels
65 QAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVF-NEVASW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dow AgroSciences LLC Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,987A
FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.1%; Score 118.5; DB 4;
24.5%; Pred. No. 3.2e-05;
tive 47; Mismatches 139;
                                                                                 116 ATLTLEDEAHTLSLLRRGDVLGAVTREANPVAGCEV----
                                                                                                                                                                                                                                                                                                                                                                        S-09-036-987A-22
Sequence 22, Application US/09036987A
Patent No. 6143526
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION
TELEPHONE: (317)337-4816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 278 amino acids
amino acid
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Best Local Similarity 24.5%
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (317)337-4847
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-09-036-987A-22
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 9330 Zionsvi
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                688 KGGMISLALSEEATRQRIENLH---GLSIAAVNGPTATVVSGDPTQIQELAQACEADGIR 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 REANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM------PVLRFGPKDV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       801 WYRNLRHRVGFAPAVETLATDEGFTHFIEVSAHPVLTMTLPDKVTGLATLRRED----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 111;
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.8%; Score 99.5; DB 3; Best Local Similarity 20.9%; Pred. No. 0.049; Matches 67; Conservative 35; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 EGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAG-
                                                           CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-06-66
EARLIER FILING DATE: 1998-06-06
EARLIER FILING DATE: 1998-06-06
EARLIER FILING DATE: 1998-06-06
EARLIER FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1998-02-08
EARLIER FILING DATE: 1998-02-22
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692 ALMRSLPGGGVMLSVQAPESEVA---PLLLGREAHVGLAAVNGPDAVVVSGERGHVA--- 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 TIAINADSLSTWFPPVFNEVASWG------129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                636 TQA----ALFALETALFRLLVQWGLKPDHLAGHSVGEIAAAHAAGILDLSDAAELVATRG 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 SLLRR---GDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAMPV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 LRFGPKDVLQDRDLDGRVDGPVGRR----RVS-----IVPSAEGFGEAIRRGLGWGLL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 PETQAAPMLKAGEVILLDEIPIDTPMYWQRWRLES-----RSLARL-TDAVVDAAIEG 287
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                                                                                                                                                                                                                                                                                                                          APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert
APPLICANT: Tang, Li
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-20029.00
CURRENT APPLICATION NUMBER: 0S/09/428,517
CURRENT FILING DATE: 1999-10-28
EARLIER APPLICATION NUMBER: 60/120,254
EARLIER APPLICATION NUMBER: 60/106,100
EARLIER FILING DATE: 1999-10-16
SARLIER FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Recombinant; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---AIEQILRDR-----GRKSRYLRVSHAFHSPLMEPVLEEFAEAVA----GLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.3%; Score 92.5; DB 4; Length 41 Best Local Similarity 23.3%; Pred. No. 1.7; Matches 70; Conservative 42; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: B CK, August; MAYER, Dagmar; SCHLENSOG,
TITLE OF INVENTION: Express System Which Can Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Collard & Roe, P.C.
STREET: 1077 No. 5830692thern Boulevard
           | | ||:| | | | : : ||| : : ||| : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : ||| | : : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| |
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                                                                                                                                                                                                                              Sequence 2, Application US/09428517
Patent No. 6251636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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LENGTH: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: A Repressor Protein and Gene for Regulating
TITLE OF INVENTION: Expression of Polypeptides and Its Use in the Preparation of
TITLE OF INVENTION: 2.2-Dialkylglycine Decarboxylase of Pseudomonas Cepacia
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                             --- TQAAPML 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 IVLHKEQLKLAIHKHHHLNQFAATGV----HLSQIIDEPMLLYPVSQKPNFATFIQSLFT 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.6%; Score 96; DB 1; Length 251,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.7%; Pred. No. v.vvv.,
tive 44; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
195 LQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01120.0002-01000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P: 1300 I Street, N.W., Suite 700 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLGWGLLP-----ETQ-AAPMLKAGEVILL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTLSLLRRGDVLGAVTREANPVAGCEVVELGT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/952,817
FILING DATE: 19920928
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28, Application US/07952817
Patent No. 5356796
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                       954 QAASVLRCDSPEEVPVDRPL 973
                                                                                                                                         245 KAGEVILLD --- EIPIDTPM 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Keller, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 251 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 21.7 nes 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202-408-4400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 13
CITY: Wash
STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                        US-07-952-817-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127
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APPLICANT: Labigue, Agnes
APPLICANT: Labigue, Agnes
APPLICANT: Labigue, Rebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
APPLICANTION: INVENTION: OMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
AITLE OF INVENTION: POLYPEPTIDES
CORRESPONDENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 QVLPAVPHLLNAVQVEATEP-----DGTKLVTVHDPISRENGELQEALFGSLLPVP---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 INADSLSTWFPPVFNEVASWGGATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 QRVKALEHHVGRVLVSRTQPAKATEAGEVLVQAARKMVLLQAETKAQLSGRLAEIPLTIA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ----SLDK-----FAETKEDNRIPGEILCEDECLTLNIGRKAVILKVTSKGDRP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 VELGTMRHLAIATPSL----RDAYMVDGKLDWAAMPVLRFGPKDVLQDR--DLDGR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.1%; Score 89; DB 2; Length 840; Best Local Similarity 22.1%; Pred. No. 0.36; Matches 59; Conservative 30; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUFTWARE: PC-DOS/MS-DOS
SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
                                                                        Sequence 25, Application US/08467822 Patent No. 5843460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 034
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          : 1300 I Street, N.W. Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-467-822-25
                                                                                                                                                                                                                                                                                                                                                                                                                        Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 GATLT------LRL---EDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTM 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.1%; Score 89; DB 2; Length 290; Best Local Similarity 23.6%; Pred. No. 0.071; Matches 74; Conservative 56; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Keusey, Edwin H.
REGISTRATION NUMBER: 34,361
REFERENCE/DOCKET NUMBER: BOCK ET AL.-4
TELECOMUNICATION:
TELEPHONE: (516) 365-9802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOCK ET AL. -4
                                                                                                                                                                                                                                                                                PRICADITION: 435
PRICATION NUMBER: GR19510930
FILING DATE: 24 MARCH 1995
APPLICATION NUMBER: GR19514056.7
FILING DATE: 13 APRIL 1995
ATTORNEY/AGENT INFORMATION:
NAME: COLIBAC, Allison C.
REGISTRATION NUMBER: 22,532
REFERENCE/DOCKET NUMBER: BOCK ET AL
ATTORNEY/AGENT INFORMATION:
NAME: Freedman, Edward R.
REGISTRATION NUMBER: BOCK ET AL
ATTORNEY/AGENT INFORMATION:
NAME: Freedman, Edward R.
REGISTRATION NUMBER: 26,048
REFERENCE/DOCKET NUMBER: BOCK ET AL
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                APPLICATION NUMBER: US/08/614,686A
FILING DATE: MARCH 12, 1996
                                                                                       MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect Version 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNDANISM: Klebsiella terrigena
STRAIN: DSM2867
14-60:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (516) 365-9802
TELEFAX: (516) 365-9805
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 290 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                     COMPUTER READABLE FORM:
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New York
: U.S.A.
                                                                                                                                                                                                                                       FILING DATE: M. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-614-686A-1
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223 GGNAIADGPVNETNLEAAMHAVRSRGFGHEEEKDAPEGFTKEDPNCSFNTFIHRKEYANK 282
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                                                                                                                                                                                                                                                                                                       APPLICANT: Kwamena A Aidoo
APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TILLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        5: JACOBSON, PRICE, HOLMAN & STERN, PPLC
The Jenifer Buliding, 400 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.0%; Score 87.5; DB 4;
33.7%; Pred. No. 0.19;
live 16; Mismatches 38;
  ----VDGPVGRRRVSIVPSA---EGFGEAIRRGLGWGLLPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1418/P57452US2
                                                                                --TQAAPMLKAGEVILLDEIPIDTPMY 262
                                                                                                                     283 YGPTTGDKIRLGDTNLLAEIEKDYALY 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08/790,462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 AARKMVLLQAE-TKAQLSGRLAEIPL 90
                                                                                                                                                                                                                  Sequence 10, Application US/09385028
Patent No. 6232106
GENERAL INFORMATION:
APPLICANT: Susan E. Jensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 141
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 39305350
TELEEX: RC 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 amino acids
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Best Local Similarity 33.7%
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                                                                                                                     US-09-385-028-10
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204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                    223 GGNAIADGPVNETNLEAAMHAVRSRGFGHEEEKDAPEGFTKEDPNCSFNTFIHRKEYANK 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 QVLPAVPHLLNAVQVEATEP-----DGTKLVTVHDPISRENGELQEALFGSLLPVP---- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 INADSLSTWFPPVFNEVASWGGATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |20 ----SLDK-----FAETKEDNRIPGEILCEDECLTLNIGRKAVILKVŢSKGDRP----- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 VELGTMRHLAIATPSL----RDAYMVDGKLDWAAMPVLRFGPKDVLQDR---DLDGR---- 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 IQVGSHYHFIEVNPYLJFDRRKAYGM--RLNIAAGTAVRFEPGDCKSVJLVSIEGNKVIR 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 QRVKALEHHVGRVLVSRTQPAKATEAGEVLVQAARKMVLLQAETKAQLSGRLAEIPLTIA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                   APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Farrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
----VDGPVGRRRVSIVPSA---EGFGEAIRRGLGWGLLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/CDCKET NUMBER: 03495.0137-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.1%; Score 89;
22.1%; Pred. No.
                                                                                                                     283 YGPTTGDKIRLGDTNLLAEIEKDYALY 309
                                                                              238 --TQAAPMLKAGEVILLDEIPIDTPMY 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/432,697
                                                                                                                                                                                                 US-08-432-697-25
Sequence 25, Application US/08432697
Patent No. 6248330
GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 22.1%
Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE; protein US-07-689-008-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 RNLNFRTLNPRIRIEGTALALATEPVPWPRTGRTRFAGVSSFGMSGTNAHVVLEEAP--- 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 VLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRLEDEAHTLS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WVDGKLDWAAMPVLRF-----GPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        546 AVRGRASGGSAPKVVFVFPFQQGSQWVGMGRKL.--MAEEPVFR-----AALEGCDRAIEA 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLGWGLLPETQA------APMLKAGEVILLDEIPIDTPMYWQRWRLESRSLAR 275
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TITLE OF INVENTION: METHODS AND NUCLEIC ACID SEQUENCES FOR THE
TITLE OF INVENTION: EXPRESSION OF CELLULOSE SYNTHASE OPERON
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3798;
                                                                            APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Sirle, Ross
APPLICANT: Cirle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 117;
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6.0%; Score 87.5;
Best Local Similarity 22.2%; Pred. No. 5.3
Matches 82; Conservative 29; Mismatches
                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/335,409
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----VGRVLVSRTQPA----
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                     Sequence 6, Application US/09335409
Patent No. 6121029
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Patent No. 5268274
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Sorangium cellulosum
US-09-335-409-6
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Calhoon, Roger D
Fear, Anna L
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Meade, James H
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                                                                                                                                                                                                                                  FILE REFERENCE: 4-30582A
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APPLICANT: Ben-Ba
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                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3798
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APPLICANT:
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US-09-335-409-6
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US-07-689-008-2
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2120 LLAGLSPADYSPAIRSIAEEMEIKODLASRLSMVSNPVPLIREALTQPDPTGARGVAVAD 2179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2288 PEA-----TSPKLALA--RLYNGHGKPGKALEIDLAVLRHNPQDLDARQAAVQAAVN 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2338 SDHNSLATRLAMDGVQESPMDARAWLAMAVADQADGHGQRTIEDLRRAYDLRLQQVEGTR 2397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 AAR-----KMYLLQAETKAQLSGRLAEIPLTIAINAD---SLSTWFPPVFNEVAS-- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 ------WGGATLTLRLEDEAHTLSLLRRG-----DVLG------AVTREAN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 PVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAMPVLRFGPKD-----VL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TQPAKATEAGEVLVQ 65
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Patent No. 5356796
GENERAL INFORMATION:
APPLICANT: Keller, John W.
TITLE OF INVENTION: A Repressor Protein and Gene for Regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 86.5; DB
Pred. No. 4.9;
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 QDRD-----LDGRVDGPVGRR---RVSIVPSAEGFG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 LALSISPSAVSQRVKAL -- EHHVGRVLVSR-----
                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/689,008
FILING DATE: 19910422

CLASSIFICATION: 47.
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 337,194
FILING DATE: 12-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 496,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Murphy, Lisabeth Feix REGISTRATION NUMBER: 31547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 393-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.9%;
Best Local Similarity 21.6%;
Matches 68; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 23-MAR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 340817 MACPAG SFO INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 3031 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415) 393-2286
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------GPVGRRRVSIVP--SAEGF------GEAIRRGLGWGLLPETQAAPMLKA 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             909 NREETPLFLAAWEGSYETAKVLLDHFANWDITDHMDRLPRDIAQERMHHDIVRLLDEYNL 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 SIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQAARKM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DGKLDWAAMPVLRFG------PKDVLQDR---DLDGRVD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 1.5; 44; Mismatches 106; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.8%; Score 85; DB 1; Length 1068; 21.6%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   758 AVISDFIYQGASL----HNQTDRTGETALHLAAR--YSRSDAAKR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 SLLRRGDVLGAVTREANPVAGCEVV-ELG-TMRHLAIATPSLRDAYMV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1152...2219
OTHER INFORMATION: Highly conserved ankyrin repeat
OTHER INFORMATION: region of No. 5780300ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Artavanis-Tsakonas, Spyridon
                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,210A
FILING DATE: 29-SEP-1995
CLASSIFICATION: 435
ATTORNEY/ACED.
       : Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                   7326-027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1029 WRKKSQDGKGCLLDSSGMLSPVDS 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 -----GEVILLDE----IPIDT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-113-825-2

Sequence 2, Application US/09113825

; Patent No. 6149902

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7320
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELERA: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Human N1 (TAN-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1068 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.8%
Best Local Similarity 21.6%
Matches 70; Conservative
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                            IX: USA
10036/2711
                          STREET: 1155 Av
CITY: New York
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       ADDRESSEE:
                                                                       STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-537-210A-2
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TITLE OF INVENTION: Expression of Polypeptides and Its Use in the Preparation of TITLE OF INVENTION: 2,2-Dialkylglycine Decarboxylase of Pseudomonas Cepacia NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 GEVLVQAARKMYLLQAETKAQLSGRLAEI - - - PLTIAINADSLSTWFPPVFNEVASWGGA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 TLTLRLE---DEAHTLSLLRRGD-----VLGAVTREA---------NP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 VAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAMPVLRFGPKDVLQDRDL----DGR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 WANRECVPMA---------DLAGEKLLMLEDGHCLRDQAMGFCFEAG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MNPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08537210A
Patent No. 5780300
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Mark
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY
TITLE OF INVENTION: DIFFERENTIATED CELLS USING THE NOTCH PATHWAY
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 VDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 ADEDTHFRATSL----ETLRNMVAAGSGITLLPALAVPPERKRDGVVYL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 85.5; DB 1; Length 2; Pred. No. 0.18; A4; Mismatches 113; Indels
                                                                                          ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPALIANCE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: US/07/952,817 FTI.ING DATE: 19920928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01120.0002-01000
                                                                                                                                    : 1300 I Street, N.W., Suite 700 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 0112/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 21.8%;
Matches 63; Conservative 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-07-952-817-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                            20005-3315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-537-210A-2
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                                                                                                                                                          CITY:
STATE:
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1029 WRKKSQDGKGCLLDSSGMLSPVDS 1052

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Fortini, Mark

APPLICANT:

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Patent No. 5/2002.
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Usderich, Robert J.
APPLICANT: Warsuno, Kenji
TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
TITLE OF INVENTION: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1948 -LLEASADANIQDNMGRTPLHAAVSADAQGVF-----QILIWNRATDLDARMHDGTTPL 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2120 VRSPQLHGAPLGGTPTLSPPLCSPNGYLGSLKPGVQGKKVRKPSSKGLACGSKEAKDLKA 2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2060 NREETPLFLAAWEGSYETAKVLLDHFANWDITDHMDRLPRDIAQERMHHDIVRLLDEYNL 2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 VLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGAT-LTLRLEDEAHTL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 SIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQAARKM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GPVGRRRVSIVP--SAEGF-----GEAIRRGLGWGLLPETQAAPMLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001 ILAARLAVEGMLEDLINSHADVNAVDDIGKSALHWAAAVNNV-DAAVVLLKNGANKDMQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PKDVLQDR----DLDGRVD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 SLLRRGDVLGAVTREANPVAGCEVV-ELG-TMRHLAIATPSLRDAYMV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%; Score 85; DB 1; Length 2556; 11.6%; Pred. No. 5.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                      ; Sequence 17, Application US/08185432 ; Patent No. 5750652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : (212) 790-9090
(212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 733
TELECOMMUNICATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2556 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-185-432-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                             New York
                                            RESULT 15
US-08-185-432-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            909 NREETPLFLAAMEGSYETAKVLLDHFANWDITDHMDRLPRDIAQERMHHDIVRLLDEYNL 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------GPVGRRRVSIVP--SAEGF------GEAIRRGLGWGLLPETQAAPMLKA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 SIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQAARKM 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 SLLRRGDVLGAVTREANPVAGCEVV-ELG-TMRHLAIATPSLRDAYMV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----PKDVLQDR---DLDGRVD----
                      MANÍPULATION OF NON-TERMINALLY DIFFERENTIATED CELLS USING THE NOTCH PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.8%; Score 85; DB 4; Length 1068;
21.6%; Pred. No. 1.5;
Live 44; Mismatches 106; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    758 AVISDFIYQGASL----HNQTDRTGETALHLAAR--YSRSDAAKR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1152...2219
CHER INFORMATION: Highly conserved ankyrin repeat
CHER INFORMATION: region of No. 6149902ch
US-09-113-825-2
                                                                                                        ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
SOFTWARET APPLICATION DATA:
APPLICATION NUMBER: US/09/113,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7326-027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---DGKLDWAAMPVLRFG----
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/537,210
FILING DATE: 29-58P-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GEVILLDE----IPIDT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REPERENCE/DOCKET NUMBER: 7326-
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-790-9090
TELEFX: 66141 PENNIE
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               COUNTRY, 2711
ZIF: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1068 amino acids
    Matsuno, Kenji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 21.0v
70; Conservative
APPLICANT: Matsuno, Kenj
TITLE OF INVENTION: MANI
TITLE OF INVENTION: DIFF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1068 amin
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206
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Search completed: September 13, 2001, 17:52:12 Job time: 1118 sec

	Ltd.
4.5	Compugen Lt
version	- 2000
GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

September 13, 2001, 17:52:41; Search time 25.14 Seconds Run on:

(without alignments)
878.704 Million cell updates/sec

US-09-105-1171-3 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: plr1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
1	538.5	36.9	303	7	G70756	hypothetical prote
7	410	28.1	300	~	B83100	4
m	376.5	25.8	297	7	S22098	replication intiti
4	376.5	25.8	297	7	F85947	hypothetical prote
Ŋ	361.5	24.8	298	7	C82318	ne in
9	177	12.1	297	7	G83145	probable transcrip
7	175	12.0	300	7	D83502	probable transcrip
8	174	11.9	295	7	E83302	
6	170	11.6	310	N	E83381	probable transcrip
10	163.5	11.2	286	~	A83482	
11	156	10.7	304	7	E83495	
12	152.5	10.4		~	G83332	
13	152.5	10.4		~	D82443	transcription regu
14	151	10.3	302	ď	B82036	
15	149.5	10.2	339	~	C83290	probable transcrip
16	149	10.2	303	7	G83354	
17	148	10.1	309	N	S70535	
18	143.5	9.8	297	N	D86063	
19	143.5	9.8	305	~	F85823	
20	142.5	9.8	302	7	D64963	
21	141.5	7.6	311	7	H83174	probable transcrip
22	140.5	9.6	305	~	B47099	nitrogen, assimilat
23	140	9.6	312	~	E83624	probable transcrip
24	139.5	9.6	297	Н	RGECIY	regulatory protein
25	139	9.5	309	7	D64139	
26	138.5	9.5	305	7	G82167	transcription acti
27	138.5	9.5	306	~	T35595	probable transcrip
28		9.5	308	7	H65014	hypothetical prote
29	138	9.5	293	7	H70067	transcription regu

probable transcrip	probable transcrip	probable transcrip	probable transcrip	probable LysR-like	transcription regu	probable transcrip	probable transcrip	probable transcrip	probable transcrip	trans-activator of	regulator for metE	lysR-type transcri	hypothetical prote	transcription regu	probable transcrip
F83023	C83536	C83310	C81954	E85517	н81011	B83536	E83498	B83158	D83319	A36066	D86070	T34997	F85869	A82436	D83630
7	7	7	7	7	7	7	7	7	7	7	7	7	N	7	7
294	298	309	309	299	309	314	296	317	298	317	317	292	312	313	302
9.3	9.3	9.5	9.1	0.6	0.6	9.0	6.8	8.9	8.9	8.9	8.9	8.8	8.8	8.8	8.8
136	136	135	133	131.5	131	131	130	130	129.5	129.5	129.5	129	128.5	128.5	128
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
														,	

ALIGNMENTS

SULT	756
S	

RESULT 1

G70756
hypothetical protein Rv1985c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 20-Jun-2000
C;Date: 17-Ju1-1998
R;Date: 17-Ju1-1998
R;Date: 17-Ju1-1998
R;Date: 1998
R;Date: 1

5 Gaps 6 Length 303; Indels Query Match 36.9%; Score 538.5; DB 2; Best Local Similarity 43.1%; Pred. No. 7.8e-36; Matches 124; Conservative 49; Mismatches 106;

δλ

αq

65 QAARKMVLLQAETKAQLSGR--LAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRL 122 ΩD

δλ

EDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWA 182 123 ŏ Dp

183 A--MPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQA 240

Q

241 APMLKAGEVILLDEIPIDTPMYWQRWRLESRSLARLTDAVVDAAIEGL 288 δλ

RESULT B83100

inhibitor of chromosome initiation IciA PA4363 [imported] - Pseudomonas aeruginosa (s

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A; Map position: 62.8 min C; Function:
                                                                          1-297 <THO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                             A; Molecule type: DNA
JN0079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: iciA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: iciA
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                                                                                                                   M.J.; Br
K.; Lim,
                                                                                                                                                                                                                                                                        A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X73026; NID:g405638; PIDN:CAA51508.1; PID:g405639
R;Thoeny, B.; Hwang, D.S.; Fradkin, L.; Kornberg, A.
Proc. Natl. Acad. Scl. US.A. 88, 4066-4070, 1991
A;Title: iciA, an Escherichia coli gene encoding a specific inhibitor of chromosomal ini A;Reference number: JN0079; MUID:91239508
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-300 <STO>
A; Cross-references: GB:AE004852; GB:AE004091; NID:g9950587; PIDN:AAG07751.1; GSPDB:GN001
A; Experimental source: strain PAO1
C; Genetics:
A; Gene: iciA; PA4363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C. Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 31-Mar-2000 C. Accession: $22098; $37499; JN0079; P$0203; C65076 R; R; Roll 1992 R; S1499; JN0079; P$0203; C65076 R; R; Leadlay, P.F. submitted to the EMBL Data Library, June 1992 A; Reference number: $22096 A; Reference number: $22096 A; Reference number: $22096 A; Reference number: $22096 A; Cross references: EMBL:X66836; NID:942941; PIDN:CAA47310.1; PID:942944 A; Rolecule type: DNA A; References: EMBL:X66836; NID:942941; PIDN:CAA47310.1; PID:942944 B; Hove-Jensen, B.; Maigaard, M. submitted to the EMBL Data Library, April 1993 A; Reference number: $37499 A; Reference number: $37499 A; Status: preliminary A; Molecule type: DNA A; Redidues: 1-176 A; Cross reference number: $37499 A; Status: preliminary A; Molecule type: DNA A; Redidues: 1-176 A; A; Cross reference number: A; Reference number: A; Rolecule type: DNA A; Redidues: 1-176 A; Rolecule type: DNA A; Redidues: Rolecule type: DNA A; Rolecule type: DNA A; Redidues: Rolecule type: Role
                                                                                                                   Hickey,
Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                            C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B83100 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hick adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replication intitiation inhibitor iciA - Escherichia coli
N;Alternate names: chromosome replication initiation inhibitor A
C;Species: Escherichia coli
A;Variety: strain K12-38
A;Variety: strain K12-38
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 31-Mar-2000
C;Accession: S22098; S37499; JN0079; PS0203; C65076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AARKMVLLQAETK ---AQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 HVQQVRLLEGDLQRWVPNLDEGGAPERLRIALNADSLATWWAAAVGDFCAERRVLLDLVV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 EDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDG--KLD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 WAAMPVLRFGPKDVLQDRDL-DGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LAALAAVVEQGGFERAAQALGLSQSAVSQRIKLLEARVGQPVLVRETPPHPTDLGRRLLN 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 AAPMLKAGEVI-LLDEIPIDTPMYWQRWRLESRSLARLTDAVVDAAIEGL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 VQGELARGELVELLPGQVIDVPLYWHYWRNGGELLASLTEHLLARAGDGL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 28.1%; Score 410; DB 2; La
Best Local Similarity 36.9%; Pred. No. 1.5e-25;
Matches 107; Conservative 47; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 410; D
Species: Pseudomonas aeruginosa
                                                                                                                                                                                          7, S.; Olson, M.V. 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary
                                                                                                                                                                                                                                                                                                                                                       A; Accession: B83100
A; Status: prelimina
                                                                                                                                                                                                      Lory,
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A;Molecule type: DNA
A;Residues: 1-297 <BLAT>
A;Cross_references: GB:AE000375; GB:U00096; NID:g1789282; PIDN:AAC75953.1; PID:g17892
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
                                                                                                                                                                    Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.J.; May
K.; Apoda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: binds to the origin (oriC) of Escherichia coli DNA to block initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-297 <STO>
A;Cross_references: GB:AE005174; NID:g12517445; PIDN:AAG58042.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
                                                                              A; Molecule type: protein
A; Residues: 1-28, 'X', 30-35, 'X', 37-38, 'XX', 41 <TH2>
R; Blattner, F.R; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley,
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1455-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID: 97426617
A; Reference number: C65076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A:Reference number: A68480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: F85947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 -PVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPM 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 AARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRLEDE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 LLRQVELLEEEWLGDEQTGSTPLLLSLAVNADSLATWLLPALAPVLADSPIRLNLQVEDE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 AHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 APVVAFDHLDDMHQAFLQQNFDLPPGSVPCHIVNSSEAFVQLARQGTTCCMIPHLQIEKE 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M62865; NID:g146435; PIDN:AAA62780.1; PID:g146436
A;Accession: PS0203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein iciA [imported] - Escherichia coli (strain 0157:H7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 LKAGEVILLDEIPIDTP-----MYWQRWRLESRSLARLTDAVVDAAIEGLR 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: regulatory protein ampR
C;Keywords: DNA binding; DNA replication inhibitor
F;21-40/Region: helix-turn-helix motif
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A;Cross-references: GB:AE004817; GB:AE004091; NID:g9950181; PIDN:AAG07382.1; GSPDB:GN A;Experimental source: strain PA01
C;Genetics:
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A; Cross-references: GB:AE004544; GB:AE004091; NID:99947060; PIDN:AAG04530.1; GSPDB:GN
                                                    probable transcription regulator PA3995 [imported] - Pseudomonas aeruginosa (strain C; Species: Pseudomonas aeruginosa (c) Species: Pseudomonas aeruginosa (c) Species: Pseudomonas aeruginosa (c) Species: Specie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable transcription regulator PAll41 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa (species: Pseudomonas aeruginosa (c;Species: Pseudomonas aeruginosa (c;Species: Pseudomonas aeruginosa (c;Species: Pseudomonas aeruginosa (september 15-Sep-2000 #sequence_revision 15-Sep-2000 #sequence_revision: D83502 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J. adman, S.; Yudan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, R.; Nature 406, 959-964, 2000
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A;Accession: D83502
A;Status: preliminary
A;MOID:20437337
                                                                                                                                                                                                                                                                                                                              A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A:Reference number: A82950; MUID:20437337
A:Accession: G83145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 -TPSL-RDAYMVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFG 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 PEPCVYREAAIT -- ALGAAARPW----RLVFESASMAGCLSAALAGFAVTVVARSQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 -GGATLTLRLEDEAHT----LSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44;
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Best Local Similarity 28.0%; Pred. No. 7.1e-07;
Matches 78; Conservative 38; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 EAIRRGL-----GWGLLPETQ-----AAPMLKAGEVI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 175;
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C, Superfamily: hypothetical protein b1875
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C, Genetics:
A, Gene: PAI1
C, Superfamily: hypothetical protein b1875
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A; Residues: 1-297 <STO>
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-298 < HEL>
A; Cross-references: GB: AE004134; GB: AE003852; NID: 99654900; PIDN: AAF93655.1; GSPDB: GN001
A; Experimental source: serogroup 01; strain N16961; blotype El Tor
C; Genetics
A; Genetics
A; Map position: 1
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                                                                                                                                                                                                                                                                                                          66 AARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRLEDE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -PVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPM 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 APVVAFDHLDDMHQAFLQQNFDLPPGSVPCHIVNSSEAFVQLARQGTTCCMIPHLQIEKE 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 AHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 DEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAA 183
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                                                                                                                                                                             6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQ 65
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                                                                     15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 298;
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                                                                     Indels
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; Score 376.5; DB 2;
; Pred. No. 7.3e-23;
53; Mismatches 125;
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25.8%;
ilarity 34.1%;
Conservative 5
                                  Best Local Similarity
                                                                 Matches 100;
Query Match
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DB 2; Length 300;

12.0%;

Match

Query

OY 266 WRLESRSLARLTDAVV 281 	RESULT 9 E83381 probable transcription regulator PA2123 [imported] - Pseudomonas aeruginosa (strain P C; Species: Psep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C; Accession: E83381 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A; Reference number: A82950; MUID:2043737 A; Accession: E83381 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-310 CSTO> A; Residues: 1-310	123 1y: conserved hypothetical protein HI1364 ch 11.6%; Score 170; DB 2; Length 310; 25.7%; Pred: No. 2.7e-06; 77; Conservative 37; Mismatches. 98; Indels 88; Ga LDTLLSIIDEGSFEGASLALSISPSAVSQRVRALEHHVGRVLVSRTQPAKATEAGEVLV 11.11	Oy 204 VOGPVGRRKVSIVPSAEGFGEAIRRGIGWGLLEETQAAPMIKAGEVILLDEIPIDTP 260 1
Best Local Similarity 27.2%; Pred. No. 1e-06; Matches 82; Conservative 44; Mismatches 121; Indels 54; Gaps 12; Qy 6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHYGRVLVSR-TQPAKATEAGEVLV 64	65 QAARKWULQAETKAQLSGRLABIPLTIAINADSLSTWFPPVENEVASW	RESULT 8 E83302 Probable transcription regulator PA2758 [imported] - Pseudomonas aeruginosa (strain PA01 C; Species: Pseudomonas aeruginosa C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C; Accession: E83302 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000 A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathchartic pathchartic pression: E83302 A; Status: preliminary A; Molecule type: DNA A; Status: Preferences: GB: AE004091; NID: 99948825; PIDN: AAG06146.1; GSPDB: GN001 C; Genetics: A; Gene: PA2758	Query Match Best Local Similarity 25.3%; Pred. No. 1.2e-06; Best Local Similarity 25.3%; Pred. No. 1.2e-06; Matches 80; Conservative 48; Mismatches 112; Indels 76; Gaps 15; Qy 6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEAGEVLV 64 :: :::

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transcription regulator LysR family VCA0575 [imported] - Vibrio cholerae (strain N169 C; Species: V1brio cholerae (c; Species: V1brio cholerae) (c; Species: V1brio cholerae; V1brio cholerae; V1brio C; Species: V1brio C; Species: V1brio Cholerae. V1brio V1brio Cholerae. V1brio Cholerae
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A;MoLeouel type: DNA
Residues: 1-292 cSTO>
A;Cross-references: GB:AE004677; GB:AE004091; NID:g9948548; PIDN:AAG05885.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337
A;Accession: G83332
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A,Residues: 1-295 <HBIN
A;Cross-references: GB:AE004388; GB:AE003853; NID:g9657979; PIDN:AAF96477.1; GSPDB:GN
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                         Drobbble transcription regulator PA2497 [imported] - Pseudomonas aeruginosa (strain probbble transcription regulator PA2497 [imported] - Pseudomonas aeruginosa (Spacies: Pseudomonas aeruginosa (C.)Spacies: Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 (Spacession: GB3322 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J. adman, S.; Yudan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 EDEA----HTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AIRRGLGWGLLP------ETQAA-PMLKAGEVILLDEIPIDTPMYWQRW 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 IQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQ-PAKATEAGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 LDW---AAMPVLRFGPKDVLQDRDLDGRVDGPVGR-RRVSIVPSAEGFGE--
    228 QTMRDAAVRGLGLAMLPLFIAAEDLAAGRLVEALPQERPLDDLIY 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 10.4%; Score 152.5; DB 2; 1.1 Similarity 25.9%; Pred. No. 6.4e-05; 84; Conservative 41; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: PA2497
C;Superfamily: hypothetical protein b1875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain PAO1
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Best Local Similarity
Matches 84; Conserva
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    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable transcription regulator PA1201 [imported] - Pseudomonas aeruginosa (strain PAO]
                                                                                                                                                                                                                                . :5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 GEVLVQAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------RVSI-VPSAEGFGEA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PLEELDQQIMVLREPGSITRRTFDRACAEQGVQPRVLLELDSREAVTEA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAARKMVLLQ-----AETKA----QLSGRLAEI-PLTIAINADSLSTWFPPVFNE-VASW 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 GGATLTLRLEDEAHTLSLLRRG-DVLGAVTR--EANPVAGCEVVELGTMRHLAIATPSLR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRLEVVLQLDD--RIVDFEKEGYDLAIRITRLQDSSLIAR----QLGTSRRVVCCSPEYL 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
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                                                                                                                                          Length 286;
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                                                                                                                                      Query Match 11.2%; Score 163.5; DB 2; Best Local Similarity 27.7%; Pred. No. 8.1e-06; Matches 74; Conservative 32; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.7%; Score 156; DB 2; 26.7%; Pred. No. 3.5e-05;
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Superfamily: conserved hypothetical protein HI1364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 VAAELGVGVVSSLEVGNDPRVRAVPLV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 IRRGLGWGLL------PETQAAPML 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Pseudomonas aeruginosa
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Matches 76; Conservative
A; Gene: PA1309
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SRTRL 313
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R; Heddelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E. J. R.R.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833
A; Accession: B82036
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-302 <HBI>A; Residues: 1-302 <HBI>A; Residues: 1-302 <HBI>A; Coss-references: GB:AE004342; GB:AE003852; NID:g9657358; PIDN:AAF95899.1; GSPDB:GN001
A; Genetics:
A; Genetics:
A; Genetics:
A; Geneticn: C; Superfamily: probable transcription regulator ybbS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription regulator LysR family VC2760 [imported] - Vibrio cholerae (strain N16961
                                                                                                                                                        17;
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Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
Accession: B82036
                                                                                                                                                                                                                                                                         ATEAGEVLVQAARKMVLLQAETK----AQLSGRLAEIPLTIAINADSLSTWFPP---VFN 108
                                                                                                                                                                                                                                                                                                          FTEAGKLILERGR--AILAATEKLVNDATLLANGWELDITIALDG-----IVPAANLFP 112
                                                                                                                                                                                                                                                                                                                                                   EVASWGGATLT-LRLEDE--AHTLSLLR--RGDVLGAVTREANPVAGCEVVELGTMRHLA 163
                                                                                                                                                                                                                                                                                                                                                                         --LRDAY----MVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |---RQPRLTVSNLDAKCKALVAGLGIGTLPLQVAQPYIDKGELKAIHGSEDLEMDIVLAW 272
                                                                                                                                                        Gaps
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                                                                                                                                                                                                                     2 LSPITLEA-LHILDAIERRGSFAAAANELNRAPSSLSYQIQKLEQDLDLMIFDRSGHRAN 60
                                                                                                                                                                                          1 MNPIQLDTLLSIID----EGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAK 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 VAAPTHYVHRRSGEFNEEAREKYRAIAIADTAREQPAMSV-----NILO------
                                                                                                                                                      67;
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                                                                                                                 Length 295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.3%; Score 151; DB 2; Length 302
26.1%; Pred. No. 8.8e-05;
.ive 53; Mismatches 118; Indels
                                                                                                                                                      Indels
                                                                                                                               Best Local Similarity 25.5%; Pred. No. 6.4e-05;
Matches 79; Conservative 62; Mismatches 102;
                                                                                                                 DB 2;
              A;Gene: VCA0575
A;Map position: 2
C;Superfamily: probable transcription regulator ybbs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Map position: 1 Superfamily: probable transcription regulator ybbS
                                                                                                             10.4%; Score 152.5; DB 25.5%; Pred. No. 6.4e-05
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Best Local Similarity 26.15
Matches 69; Conservative
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RRNQMGEAKS 282
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C; Genetics
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Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Joson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa·PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337
A;Accession: C83290
A;Accession: C83290
A;Accession: C8290
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable transcription regulator PA2848 [imported] - Pseudomonas aeruginosa (strain C; Species: Pseudomonas aeruginosa C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C; Accession: C83290 R; Stover, C.K.; Pham, X.O.: Erwin, A.T.: Wiscanschife C. A.T.: Pham, A.O.: Erwin, A.D.: Pham, A.D.: Pham, A.O.: Erwin, A.D.: Pham, A.D.: Pha
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174 MVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWG
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C;Superfamily: conserved hypothetical protein HIl364
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

September 13, 2001, 17:57:09

% Search time 15.26 Seconds
(without alignments)
650.989 Million cell updates/sec

US-09-105-1171-3 1460 1 MNPIQLDTLLSIIDEGSFEG.....RSLARLTDAVVDAAIEGLRP 290 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	P94632 corynebacte		P24194 escherichia	O52399 edwardsiell			-		-		-			P19797 escherichia	P10086 alcaligenes		P52678 mycobacteri	P36771 escherichia			. P42722 alcaligenes		P51205 porphyra pu	-	_			_	-	•	33	7702	Q50683 mycobacteri
SUMMARIES		ID	LYSG_CORGL	YJ85_MYCTU	ICIA_ECOLI	ICIA_EDWIC	ICIA_AERSA	LTRAKLEPN	NAC_ECOLI	NAC_KLEAE	ILVY_ECOLI	METR_HAEIN	YFER_ECOLI	METR_SALTY	LRRA_SYNP7	METR_ECOLI	TFDR_ALCEU	ESTR_ACICA	OXYR_MYCLE	LRHA_ECOLI	BLAA_STRCI	NTCB_SYNP7	CFXR_ALCEU	PECT_ERWCH	YC30_PORPU	YDHB_ECOLI	TRPI_PSESY	OPRR_PSEAE	CBBR_RHORU	OXYR_MYCAV	YEAT_ECOLI	HVRB_RHOCA	YCJZ_ECOLI	YBBS_ECOLI	YM82_MYCTU
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æ	Query	Match	100.0			25.0			8.6					9.3		•	8.8	8.7			8.7	٠.	•		9.6				•	7.9		7.6	7.6	7.4	7.4
		Score	9	538.5		365.5	355.5	-		140.5	139.5	139	138.5	136.5	m	129.5	128	127.5	127.5	127.5	127.5	126.5	126.5	126	125.5	121	117.5	116.5	115.5	115.5	111.5	111	111	108.5	108
	Result	. No.	1	61	m	4	S	φ	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

escherichia	synechocyst	haemophilus	rhizobium s	agrobacteri	bacillus su	pseudomonas	bacillus su	bacillus su	rhodobacter	enterobacte	escherichia
P42623	P74422	P44821	P55576	P52669	034827	005840	P39647	035038	P52690	P52665	P27111
YHAJ_ECOLI	NTCB_SYNY3	ILVY_HAEIN	Y4MQ_RHISN	TUA4_AGRVI	YKUM_BACSU	CLCR_PSEPU	YWFK_BACSU	YTLI_BACSU	CBBR_RHOSH	BUDR_ENTAE	CYNR_ECOLI
7	٦	Н	-	Н	-4	٦	٦	Н	-	٦	Н
298	309	292	298	304	293	294	299	308	310	143	299
7.4	7.4	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.2	7.2
•	107.5 7.4	• -	• -				•			•	

ALIGNMENTS

STANDARD; PRI; 290 AA.	P94632; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) LYSINE EXPORT TRANSCRIPTIONAL REGULATORY PROTEIN LYSG.	LYSG. Corynebacterium glutamicum (Brevibacterium flavum). Bacteria: Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-97126810; Pubmed-8971704; Varlio M., Sahm H., Eggeling L.; An new type of transporter with a new type of cellular function: L- 1ysine export from Corynebacterium glutamicum.";	MOL. MICTODIOL. 27:815-826(1996). -!- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR OF LYSE. -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	TENT B74	Match Ocal Similarity 100.0%; Score 1460; DB 1; Length 290; S 290; Conservative 0; Mismatches 0; Indels 0; Gaps 1 MNPIQLDTLLSIIDEGSFEGASIALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAG 60	
	71998 (Rel. -1998 (Rel. -1998 (Rel. EXPORT TRAN	LYSG. Corynebacterium c Bacteria; Firmicu Actinomycetales; Corynebacterium.	[1] SEQUENCE FROM N.A STRAIN-R127; MEDLINE-97126810; Vrljic M., Sahm H "A new type of tra lysine export from	MICTODIOL. FUNCTION: PRC SIMILARITY: E REGULATORS.	This SWISS-PROT ebetween the Swisther the European Biologuse by non-profuse modified and this entities requires or send an email	EMBL; X96471; CAA6532 InterPro; IPR000847; Pfam; PF00126; HTH-1; PROSITE; PS00044; HTH DNA-binding; Transcri DNA_BIND 18 SEQÜENCE 290 AA; 3	Ouery Match Best Local Similarity Matches 290; Conserv 1 MNPIQLDTLESIII	MINE TOLD I LIGHT I LIBERGE EGRALIANIA STANDONNY MALBANIANA I VARANTERA EVIVOAARKWYLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTL
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                                                                                  EDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWA 182
                                                                                                                                                                                       A--MPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQA 240
                                                                                                                                                                                                                                                               AAKAPSLAWNRDDGLQDM-LVRKAFRRAITRPTHFVPTTEGFTAAARAGLGWGMFPEKLA 245
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"Escherichia coli rpiA gene encoding ribose phosphate isomerase A.";
J. Bacteriol. 175:5628-5635(1993).
-1- FUNCTION: SPECIFIC INHIBITOR OF CHROMOSOMAL INITIATION OF
REPLICATION IN VITRO. BINDS THE THREE 13-MERS IN THE ORIGIN
(ORIC) TO BLOCK INITIATION OF REPLICATION.
-1- SUBUNIT: BEHAVES AS HOMODIMER IN SOLUTION.
REGULARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 1-41.
STRAIN=K12 / W3110;
MEDLINE=91239508; PubMed=2034653;
MEDLINE=91239508; S., Fradkin L., Kornberg A.;
"iciA, an Escherichia coli gene encoding a specific inhibitor of chromosomal initiation of replication in vitro.";
Proc. Natl. Acad. Sci. U.S.A. 88:4066-4070(1991).
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STAIN-KIZ / MGIG55;
MEDIJNE=97426617: PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CHROMOSOME INITIATION INHIBITOR (ORIC REPLICATION INHIBITOR)
                                                                                                                                                                                                                                                                                                                                  241 APMLKAGEVILLDEIPIDTPMYWQRWRLESRSLARLTDAVVDAAIEGL 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roy I., Leadlay P.F.; Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                        246 ASPLADGSFVRVCDIHLDVPLYWQCWKLDSPIIARITD-TVRAAASGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICIA_ECOLI
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ICIA_ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5,
                                                                                                                    240
181 WAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ö.
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 QLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.I. "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."

"Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).

"Indianal C. Station S., Station S., Squares S., Sulston J.I. Similanity: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                WAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 303;
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Hypothetical protein; Transcription regulation; DNA-binding.
DNA_BIND 23 42 H-T-H MOTIF (POTENTIAL).
SEOUENCE 303 AA; 32836 MW; 3448DB1056207144 CRC64;
                                                                                                                                                                                                                                                                                                241 APMLKAGEVILLDEIPIDTPMYWQRWRLESRSLARLTDAVVDAAIEGLRP 290
                                                                                                                                                                                                                                                       241 APMLKAGEVILLDEIPIDTPMYWQRWRLESRSLARLTDAVVDAAIEGLRP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.9%; Score 538.5; DB 1; Length 43.1%; Pred. No. 3.8e-36; Live 49; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR RV1985C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-H37RV;
MEDLINE-98295987; PubMed-9634230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RV1985C OR MTCY39.34
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Pfam; PF00126; HTH_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGULATORS.
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Q10872;
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EMBL; M62865; AAA62780.1; -.

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Query Match Local

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REGULATORS
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P70773;
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                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                      189 APVVAFDHLDDMHQAFLQQNFDLPPGSVPCHIVNSSEAFVQLARQGTTCCMIPHLQIEKE 248
                                                                                                                                                                                                                                                                                                                       66 AARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRLEDE 125
                                                                                                                                                                                                                                                                                     69 LLRQVELLEEEWLGDEQTGSTPLLLSLAVNADSLATWLLPALAPVLADSPIRLNLQVEDE 128
                                                                                                                                                                                                                                                                                                              126 AHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM- 184
                                                                                                                                                                                                                                                                                                                                                         185 -PVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPM 243
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                       6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                    244 LKAGEVILLDEIPIDTP------MYWQRWRLESRSLARLTDAVVDAAIEGLR 289
                                                                                                                                                                                                                                                                                                                                                                                                                 249 LASGELIDL-----TPGLFQRRMLYWHRFAPESRMMRKVTDALLDYGHKVLR 295
                                                                                                                                                                            Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CHROMOSOME INITIATION INHIBITOR (ORIC REPLICATION INHIBITOR)
                                                                                               PRINTS; PRO0039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR.FAMILY: 1.
DNA-binding; Transcription regulation.
DNA_BIND 40 40
SEQUENCE 297 AA: 33471 MW; BAD60B76661E3EF CRC64;
                                                                                                                                                                                                   Indels
                                                                                                                                                                            25.8%; Score 376.5; DB 1; 34.1%; Pred. No. 3.5e-23;
                                                                                                                                                                                                  53; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 AA.
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30-MAY-2000 (Rel. 39, Last sequ
30-MAY-2000 (Rel. 39, Last anno
                    AE000375; AAC75953.1;
                               X73026; CAA51508.1;
                                                                                                                                                                                       Best Local Similarity 34.19
Matches 100; Conservative
                                        PIR; JN0079; JN0079.
PIR; S22098; S22098.
EccGene; EC10490; iciA.
InterPro; IPR000847; -.
Pfam; PF00126; HTH_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
          U28377; AAA69083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Edwardsiella ictalur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=67780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=93-146;
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052399;
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                       EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 LLHQVELLEEEWLGNDNSSDGPLLLSLAVNADSLATWLLPALKPVLADSPLRLNLQVEDE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 MPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPM 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AARKMVILQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRLEDE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 AHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDG--KLDWAA 183
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 APAVAFDHLDDMHQAFLQQNFELPPGSVPCHIVNSSEAFVQLALQGTTCCMLPHLQVERE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CHROWOSOME INITIATION INHIBITOR (ORIC REPLICATION INHIBITOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 LKAGEVILLDEIPIDTP-----MYWQRWRLESRSLARLTDAVVDAAIEGLR
                                                                                                                                                               H-T-H MOTIF (BY SIMILARITY). 93BEC456B2419989 CRC64;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                       25.0%; Score 365.5; DB 1; 33.4%; Pred. No. 2.6e-22; ive 51; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 AA
                                                                           PRINTS; PR00039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
DNA-binding; Transcription regulation.
DNA_BIND 21 40 H-T-H MOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00126; HTH_1; 1.
PRINTS; PR00039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR_FAMILY;
                                                                                                                                                                                        297 AA; 33392 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U65741; AAB70016.1; -. InterPro; IPR000847; -.
EMBL; AF037440; AAB92569.1;
InterPro; IPR000847; -.
Pfam; PF00126; HTH_1; 1.
                                                                                                                                                                                                                                                                                                     Similarity 33.4% 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aeromonas.
NCBI_TaxID=645;
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48; Gaps

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MEDLINE-98155143; PubMed-9495755;
Muse W.B., Bender R.A.;
"The nac (nitrogen assimilation control) gene from Escherichia coli.";
J. Bacteriol. 180:1166-1173(1998).
                                                                                                                                                                                                                                                                                                                                                        OHAQOMLEAARQAMDSAGSRQTVAQGKLTLSVPKAVGRFVIHPLMMAFFHRYPQVDVCLR 128
                                                                                                                                                                                                                                      LEDEAHTLSLLRRG-DVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLD 180
                                                                                                                                                                                                                                                                               LED--RPLDFIDDGIDLALRITDTPSP--GLHGKPLMPIRHVICAT----EAY----LQ 175
                                                                                                                                                                                                                                                                                                                              WAAMPVLRFGPKDV------LQDRDLDGRVDGPVGRRRVSIVPSAEGFG------ 223
                                                                                                                                                                                                                                                                                                                                                                                                                      224 -EAIRRGLGWGLLPETQAAPMLKAGEVI-LLDE---IPIDTPMYWQRWRLESRSLARLTD 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                229 LDAVRQHLGIGSLPLFTAREALANGDIVQVLPEWEFISSYSGDLWLLWAGDKHMPARMR- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            res. 3:3/9-392(1990).
FUNCTION: TRANSCRIPTIONAL ACTIVATOR FOR THE HUT, PUT AND URE OPERONS AND REPRESSOR FOR THE GDH AND GLTB OPERONS IN RESPONSE TO
                                                                                                                                              QAARKMV--LLQAETKAQLSGRLAEIPLTIAI-NADSLSTWFPPVFNEVASWGGATLTLR 121
                                                                                   LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAGEVLV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT--2000 (Rel. 40, Last annotation update)
NITROGEN ASSIMILATION REGULATORY PROTEIN NAC (NITROGEN ASSIMILATION
CONTROL PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE=97426613;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.
Blattner F.R., Plunkett G. III, Bloch C.A., Rose C.K., Mayhew G.F.,
Riby M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97251358; PubMed=9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H.,
Takeda J., Takemoto K., Wada C., Yanamoto Y., Horiuchi T.;
Takeda J., Takemoto K., Wada C., Yanamoto Y., Horiuchi T.;
Takeda J., Takemoto K., Mola C., Yanamoto Y., Horiuchi T.;
Takeda J., Takemoto K., Mola C., Yanamoto Y., Horiuchi T.;
DNA ROS. 3:379-392(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
         Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
         50;
           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 AVVD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 AMID 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia.
         80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAC_ECOLI
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           Matches
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                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                        74 RQLELE----LAGEIAPDEPQAPIRVSIAVNADSLATWFLPALAPLLEQHPIELNLLVDD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAA 241
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                      VLLQAETKAQLSGRL-----AEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRLED 124
                                                                                                                                                                                                                                                                                                                                                                                                   EAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAM 184
                                                                                                                                                                                                              11 SIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQAARKM 70
                                                                                                                                                                                                                                      14 AVWQEQNFERAAQRLHITQSAISQRIKQLEQQFAEPLLIRSQPLQATPLGQKLLAHYRQV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Klebsiella.
                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 PMLKAGEVILLDEIP---IDTPMYWQRWRLESRSLARLTDAVVDAAIEGLRP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 QQLAQG--ILLDLSPSHHLIEPLYWHRWVLERGLHKQISQRLISEGRRALQP 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Microbiol. 18:533-546(1995).-!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL.
                                                                                                                         Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bott M., Meyer M., Dimroth P.; "Regulation of anaerobic citrate metabolism in Klebsiella
                                                                                                                                                                 Indels
DNA-binding; Transcription regulation.
DNA_BIND 21 40 H.T.H MOTIF (POTENTIAL).
SFOUENCE 299 AA; 33410 MW; 5EEBECA44CC5A68D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; DNA-binding.
DNA_BIND 21 H-T-H MOTIF (POTENTIAL).
SEQUENCE 309 AA; 34357 MW; 5C54D416605C734A CRC64;
                                                                                                                      Query Match 24.3%; Score 355.5; DB 1; Best Local Similarity 33.6%; Pred. No. 1.7e-21; Matches 98; Conservative 49; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 148; DB 1;
Pred. No. 7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
PROBABLE TRANSCRIPTIONAL REGULATOR LIRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00126; HTH_1; 1.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96342382; PubMed=8748036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 40 H
309 AA; 34357 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U31464; AAC44735.1; -.
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26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000847;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 13882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGULATORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTRA_KLEPN
P52689;
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RESULT 6 LTRA_KLEPN

125

185

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                                          5
P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 TPSLR-DAYMVDGK-----LDWAAMPVLR-FGPKDVLQDRDLDGRVDGPVGRRVSI-- 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 QPLLKEDLYLVGTRDCPGQSVDLTAVAEMNLFLPRDYSAVR---ARVTEAFTLRRLSAKI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 GEVLVQAARKMVLLQAE------TKAQLSGRLAEIPLTIAINADSLSTWFPPVF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GKILYTHAR-TILKQCEQAQLAVNNVGQTLRGQVSIGLAPGTAASAITMPLLQT----VR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 NEVASWGGATLTLRLEDEAHTL--SLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: TRANSCRIPTIONAL ACTIVATOR FOR THE HUT, PUT AND URE OPERONS AND REPRESSOR FOR THE GEH AND GLFB OPERONS IN RESPONSE NITROGEN LIMITATION. NEGATIVE REGULATOR OF ITS OWN EXPRESSION. SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wek R.C., Hatfield G.W.; "Nucleotide sequence and in vivo expression of the ilvY and ilvC genes in Escherichia coli K12. Transcription from divergent overlapping promoters.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
Transcription regulation; DNA-binding; Activator; Repressor;
Nitrate assimilation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H-T-H MOTIF (POTENTIAL).
775F219AF32AFADC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 140.5; DB 1
Pred. No. 0.00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.6%; Scc. No. v.. 28.1%; Pred. No. v.. 39; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---VPSAEGFGEAIRRGLGWGLLPETQAAPMLKA 246
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSCRIPTIONAL ACTIVATOR PROTEIN ILVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
Bacteriol. 175:2107-2115(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=86111952; PubMed=3003115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 AA; 32754 MW;
                                                                                                                                                                                                                                                                                                             EMBL; L01114; AAA18173.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 20.11es 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00039; HTHLYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00126; HTH_1; 1
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000847; -.
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09,
35,
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(Rel. (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
                                                                                                      REGULATORS.
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01-NOV-1988
01-NOV-1997
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P05827;
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Best Local
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  g
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                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
  NITROGEN LIMITATION. NEGATIVE REGULATOR OF ITS OWN EXPRESSION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKILYTHAR-AILROCE-QAQLAVHNVGQALSGQVSIGFAPGTAASSITMPLLQAVRAE- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----FPEIVIYLHENSGAVLNEKLIN--HQLDM-----AVIYEHSPVAGVSSQALLK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------C--EVVELGTMRHLAIATPSLRDAYMVDGKLDWAAMPVLRFGPKDVLQDR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 GEVLVQAARKMVLLQAETKAQ-----LSGRLA------EIPLTIAINADS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-R07-1997 (Rel. 35, Last annotation update)
NITROGEN ASSIMILATION REGULATORY PROTEIN NAC (NITROGEN ASSIMILATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLDGRVDGPVGRRRVSIVPSAEGFGE------AIRRGLGWGLLPETQAAPMLKA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 EDLFLVGTODCPGOSVDVNAIAOMNLFLPS-----DYSAIRL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MNPIQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSTWFPPVFNEVASWGGATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
                   SIMILARITY).
SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schwacha A., Bender R.A.; "The nac (nitrogen assimilation control) gene from Klebsiella aerogenes.";
                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00126; HTH-1; 1.
PRINTS; PR00039; HTH-LYSR.
PROSITE; PS00044; HTH-LYSR.FAMILY; 1.
Transcription regulation; DNA-binding; Activator; Repressor; Nitrate assimilation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H-T-H MOTIF (POTENTIAL).
B0B5DC408C6C6821 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.8%; Score 142.5; DB 1;
25.3%; Pred. No. 0.00019;
tive 45; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=W70 / KC1043;
MEDLINE-93209957; Pubmed=8458853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 AA; 32835 MW;
                                                                                                                                                                                                                                                                EMBL; U56736; AAD14869.1; -. EMBL; AE000290; AAC75050.1;
                                                                                                                                                                                                                                                                                                         EMBL; D90837; BAA15806.1;
EcoGene; EG14265; nac.
InterPro; IPR000847; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=28451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONTROL PROTEIN)
                                                             REGULATORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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01-NOV-1995
                                                                                                                                                                    Haemophilus
                                         METR_HAEIN
P45349;
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                            METR_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 VFAQQTLLQYQQLRHTIDQQGPSLSGE----LHIFCSVTAAYSHLPPILDRFRAEHPSV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAARKMVLLQAETK-----AQLSGRLAEIPLTIAINADSLSTWFPPVFNEV-ASWGGA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 TLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIA--TPSL----R 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 EIKLTTGDAADAMEKVVTGEADLAIAGKPETLPG--AVAFSMLENLAVVLIAPALPCPVR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOVSVE-KPDWSTVPF-----IMADQ-----GPV-RRRIELWFRRNKISNPMIYAT 222
                                                             Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.; "Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LKTFLHLAESRHFGRSARAMHVSPSTLSRQIQRLEEDLGQPLEVRDNRTVTLTEAGEELR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAGEVLV 64
                                                                                                                                                                                                                     Escherichia coli K-12.;
Nucleic Acids Res. 15:2137-2155(1987).
-!- FUNCTION: THIS PROTEIN ACTIVATES THE TRANSCRIPTION OF THE ILVC GENE IN THE PRESENCE OF ACETOLACTATE OR ACETOHYDROXYBUTYRATE.
ILVY IS ALSO A NEGATIVE REGULATOR OF ITS OWN EXPRESSION.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 DAYMYDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSI--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00044; HTH_LYSR_PAMILX; 1.
Branched-chain amino acid biosynthesis; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 297;
                                                                                                                                                               MEDLINE-87174741; PubMed=3550695;
Lawther R.P., Wek R.C., Lopes J.M., Pereira R., Taillon B.E.
Hatfield G.W.;
                                                                                                                                                                                                            "The complete nucleotide sequence of the ilvGMEDA operon of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brancharchain amino actu processor; BNA-binding.
Activator; Repressor; DNA-binding.
nNA BIND 18 37 H-T-H MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPSAEGFGEAIRRGLGWGLLPET--QAAPMLKAGEVILLDEIPIDTP 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.6%; Score 139.5; DB 1
23.3%; Préd. No. 0.00032;
tive 50; Mismatches 115
Biol. Chem. 261:2441-2450(1986)
                         SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-92358234; PubMed-1379743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M87049; AAA67576.1; -. AE000453; AAC77493.1; -.
                                                                                                                                     SEQUENCE OF 264-297 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M11689; AAA24028.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M32253; AAA24025.1; -. PIR; B26287; RGECIY.
                                                                                             from 84.5 to 86.5 minutes. Science 257:771-778(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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InterPro; IPR000847; -.
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Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                     REGULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 QAARKMY--LLQAETKAQLSGRLAEI-----PLTIAINADSLSTWFPPVFNEVAS-WGG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLANEVMPKVIDAERD ----LARVKHGDAGQLRIAVECHTCFDWLMPAMDEFRQHWG- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATLTLRLEDEAHT----LSLLRRGDVLGAVTREA------NPVAGCEVVELGTMRHLA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
Transcription regulation; DNA-binding; Methionine biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 9.5%; Score 139; DB 1; Length 309; Best Local Similarity 26.5%; Pred. No. 0.00037; Matches 72; Conservative 45; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 42 H-T-H MOTIF (POTENTIAL).
309 AA; 35344 MW; AOC2F0277DE8B274 CRC64;
                                                                                                     Last sequence update)
Last annotation update)
Ā
                                                                                                                                                                      TRANSCRIPTIONAL ACTIVATOR PROTEIN METR
                                                                 (Rel. 32, Created)
(Rel. 32, Last seq
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                                                                                                                                                                                                                                           Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=727;
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164 IATPSLRDAYMVDGKLD--WAAMPVLRFGPKDVLQDRDLDGRV---DGPVGRRRVSIVPS 218
              coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-CT-2000 (Rel. 40, Last annotation update)
14POTHETICAL TRANSCRIPTIONAL REGULATOR IN XAPA-LIG INTERGENIC REGION.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-KIZ. 7 MG1655;
STRAIN-KIZ. 7 MG1655;
STRAIN-KIZ. 7 PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription regulation; DNA-binding. H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                           308 AA
                                                                  219 AEGFGEAIRRGLGWGLLPETQAAPMLKAGEVI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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PROSITE; PS00044; HTH LYSR.FAMILY; 1.
Hypothetical protein; Transcription ry
BONA_BIND 20 39 H-TH MO
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K12;
MEDLINE=97349980; PubMed=9205837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000328; AAC75462.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, D90870; BAA16280.1; -.
EcoGene; EG14159; yfeR.
InterPro; IPR000847; -.
                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00126; HTH_
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGULATORS.
                                                                                                                                                                                                                                    Escherichia
                                                                                                                                            YFER_ECOLI
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SEQUENCE
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18;

Gaps

63;

Query Match 9.5%; Score 138.5; DB 1; Length 308; Best Local Similarity 25.1%; Pred. No. 0.0004; Matches 78; Conservative 51; Mismatches 119; Indels 63.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ::| ::| | | | | ::| | 122 EIGHPATLFPMVAAGIGISILP-ALALP-LPEGSPLVVKRI---TPVVERQLMLVRRKNR 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 GFGE-----AIRRGLGWGLLPETQAAPMLKAGEVILLDEIPIDTPMYWQRW---RLESR 271
                                                                                                                                                         64 VQAARKMVLLQAETKA-----QLSGRLAEIPLTIAINADSLSTWFPP--VFNEVA 111
                                                                                                                                                                                                                                                                                                              112 SWGGATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAG--CEVVELGTMRHLAIATPSL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-87307964; PubMed=3040668; Plamann L.S., Stauffer G.V.; "Nuclectide sequence of the Salmonella typhimurium metR gene and the metR-metE control region."; J. Bacteriol. 169:3932-3937(1987).
                                                                          64
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1997) to the LAST STEP IN METHIONINE BIOSYNTHESIS;
METR IS A POSITIVE ACTIVATOR OF THE META, METE AND METH GENES.
METR IS ALSO A NEGATIVE REGULATOR OF ITS OWN EXPRESSION.
-!- SUBGELLULAR LOCATION: CYTOPLASMIC.
-!- SIGNELLULAR LOCATION: CYTOPLASMIC.
-!- SIGNIARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
                                     ----RD-AYMVDGKLDWAAMPVLRFGPKDVLQDRDLDGR--VDGPVGRR--RVSIVPSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVG-RVLVSRTQPAKATEAGEVL
                                                                                                                                                                                                                                    -QLALRLERLLDELNSTLRDTGRMGQQLSGKVR-----VAASQTISAHLIPQCIAESHR
                                                                                                                                                                                                                                                                                                                                                                                             118 RYPDIQFVLHDRPQQWVMESIRQGDVDFGIVIDPGPVGDLQCEAI-----LSEPFF
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InterPro; IFR000847; -.
Pfam; PF00126; HTH_1: 1.
PRINTS; PR00039; HTHLYSR.
PROSTED; PS00044; HTH_LYSR.FAMILY; 1.
Transcription regulation; DNA-binding; Methionine biosynthesis; Activator; Repressor.
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15-DEC-1998 (Rel. 37, Last sequence update)
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TRANSCRIPTIONAL ACTIVATOR PROTEIN METR.
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Anandan S., Nalty M.S., Cogdell D.E., Golden S.S.;
"Identification of two classes of transcriptional regulator genes
the cyanobacterium Synechococcus sp. strain PCC 7942.";
Arch. Microbiol. 166:58-63(1996).
-1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
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                                                                                                                            Length 317;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cus sp. (strain PCC 7942) (Anacystis nidular
Cyanobacteria; Chroococcales; Synechococcus
                                                                                                                            DB 1;
                                                                                                                                                                                      29; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 ATLTLRLEDEAHTLSLLRRGDVLGAVTREANPVAGCEV----
                                                                                                                         9.3%; Score 136.5; DB 23.9%; Pred. No. 0.0006;
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01-0CT-1996 (Rel. 34, Last sequence update)
10-CCT-1996 (Rel. 34, Last annotation update)
PROBABLE TRANSCRIPTIONAL REGULATOR LRRA
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38 H-
35585 MW;
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                                                                                                                                                Best Local Similarity 23.99
Matches 69; Conservative
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19
317 AA;
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SEQUENCE
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12;

Gaps

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Indels

87;

42; Mismatches

Conservative

Query Match Best Local Similarity Matches 68; Conserv

9.3%; Score 136; DB 1; Length 294; 23.4%; Pred. No. 0.00061;

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                                                                                                                                                                                                                                                                                                                                                                                                         -----AGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAAMPVLRFGPK 192
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STRAIN=KIZ. / MG165;
STRAIN=KIZ. / MG165;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
Daniels D.L., Plunkett G. III, Burland P.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region Science 257:771-778(1992).
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MEDLINE-89098936; PubMed=2643109;
MAXON M.E., Redfield B., Cal X.-Y., Shoeman R., Fujita K., Fisher W..
Stauffer G., Welssbach H., Brot N.;
"Regulation of methionine synthesis in Escherichia coli: effect of the MetR protein on the expression of the metE and metR genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:85-89(1989).

"HETRIS A POSITIVE ACTIVATOR OF THE LAST STEP IN METHIONINE BIOSYNTHESIS;
METR IS A POSITIVE ACTIVATOR OF THE META, METE AND METH GENES.

METR IS ALSO A NEGATIVE REGULATOR OF ITS OWN EXPRESSION. BINDS
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| GVSVSIIETDPQGVEQALREGKVDIGLLPLPRSEEFDTWEITRDEYVVLLPSTAHPLGQP
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Maxon M.E., Wigbolds J., Brot N., Weissbach H.;
"Structure-function studies on Escherichia coli MetR protein, a
putative prokaryotic leucine zipper protein.";
Proc. Natl. Acad. Sci. U.S.A. 87:7076-7079(1990).
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SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
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01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
TRANSCRIPTIONAL ACTIVATOR PROTEIN METR.
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MEDLINE-90384950; PubMed-2205852;
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"Analysis of duplicated gene sequences associated with tfdR and tfdS
in Alcaligenes eutrophus JMP134.";
J. Bacteriol. 176:2348-2353(1994).
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                                                                                                                                PIR; S30718; S30718.

BEOGGANE; EG10591; metR.

Interpro; IPR000847; -.

PRINTS; PR00039; HTHLL1; 1.

PROSTTE; PR00044; HTHLLYSR FAMILY; 1.

Transcription regulation; DNA-binding; Methionine biosynthesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                        8.9%; Score 129.5; DB 1; Length 317; 23.3%; Pred. No. 0.0022; tive 33; Mismatches 111; Indels 83
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L -> T (IN REF. 3).
513F5C710803800D CRC64;
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01-MRF-1989 (Rel. 10, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
TRANSCRIPTIONAL REGULATORY PROTEIN TDFR/JFDS.
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Alcaligenes eutrophus (Ralstonia eutropha).
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19 19 L
317 AA; 35629 MW;
                                                        EMBL; AE000458; AAC76831.1;
EMBL; J04155; AAC24159.1; -
PIR; A36066; A36066.
PIR; S30718; S30718.
                     M37630; AAA62781.1; -. M87049; AAA67624.1; -.
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DNA_BIND 19 3
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                                                                                            MEDLINE=88320486; PubMed=3413113;
Henikoff S., Haudhn G. W., Calvo J.M., Wallace J.C.;
Henikoff S., Haudhn G. W., Calvo J.M., Wallace J.C.;
Henikoff S., Haudhn G. W., Calvo J.M., Wallace J.C.;
Proc. Natl. Acad. Sci. U.S.A. 85:6602-6606(1988).
-! FUNCTION: INVOLVED IN REGULATION OF 3-CHILORCOATECHOL DEGRADATION.
-! TRANSCRIPTIONAL REGULATION OF TEDB EXPRESSION. ACTS AS A REPRESSOR IN THE ABSENCE OF ITS EFFECTOR (EITHER 2-CIS-CHLORODIENE LACTONE OR CHLOROMALEYLACETATE) BUT ACTS AS AN ACTIVATOR WHEN ITS EFFECTOR.
-! SUBCELLUAR LOCATION: CYTOPLASMIC.
-! SUBCELLUAR LOCATION: CYTOPLASMIC.
-! ADDLICATED GENE TFDR AND TFDS.
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Job time: 296 sec
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eutrophus JMP134.";
J. Bacteriol. 169:2950-2955(1987).
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces cosmids and a detailed genetic and physical map for The 8 Mb Streptomyces colloolor A3(2) chromosome.";

"A set of ordered cosmids and a detailed genetic and physical map for The 8 Mb Streptomyces colloolor A3(2) chromosome.";

"A set of ordered cosmids and TT-96(1966).

"A microroling Transcription or TRANSCRIPTIONAL REGULATORS.

"B EMBL; AL357613; CAB93745.1; -..

"A InterPro: IPR001993; -..

"B PFONT; PR001993; -..

"B PROSITE; PS00014; HTHLYSR. FAMILY; UNKNOWN.1.

"B PROSITE; PS00044; HTHLYSR. FAMILY; UNKNOWN.1.

"B PROSITE; PS00215; MITCHCH-CARRIER; UNKNOWN.1.

"B PROSITE; PS00215; MITCHCH-CARRIER; UNKNOWN.1.

"B PROSITE; PS00215; MTCHCH-CARRIER; UNKNOWN.1.

"B PROSITE; PS00215; MTCHCH-CARRIER; UNKNOWN.1.

"B PROSITE; PS00215; MTCHCH-CARRIER; UNKNOWN.1.
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Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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Seeger K.J., Harris D.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE LYSR-FAMILY TRANSCRIPTIONAL REGULATOR.
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MEDLINE=97000351; PubMed=8843436;
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                             425026 segs, 132305027 residues
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Listing first 45 summaries
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Q87968

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                                                                                                                    RLAROVARLERDASAELGLRGEGEPTRVTVAVNADSLATWFLPALTRIPREPALCFELRR 131
                                                                                                                                          EDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKL--D 180
                                                                                                                                                    EAGEVLVQAARKMVLLQAETKAQL -- SGRLAEIPLTIAINADSLSTWFPPVFNEVASWGG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 ATLTLRLEDEAHTL------SLLRRGD-VLGAVTREANPVAGCEVVELGTMR 160
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                                 Gaps
                                                                 12 QVRTLLAVVDEGTFDAAAAALHVTPSAVSQRVKALEQRTGRVLLLRTKPVRATDSGAVLV 71
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                                                     QLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLV
                                                                                                                                                                                    181 WAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQA
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                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                            Umeyama T.;
"Open reading frame encoded around afsA gene.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
EMBL; AB011413; BAA32133.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.4%; Score 472.5; DB 2; Length 303; 39.3%; Pred. No. 1.7e-28;
          Length 300;
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                                                                                                                                                                                                                                           250 EPLLRTGRLVTFAPDLAVDVTLYWQQWKLDSPALATVADAVVTAAADALR
                                                                                                                                                                                                                              241 APMLKAGEVI-LLDEIPIDTPMYWQRWRLESRSLARLTDAVVDAAIEGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: irnoull.

Pfam: PF00126; HTH_1: i.
PRINTS: PR00129; HTH_LYSR.
PROSITE; PS00044; HTH_LYSR.FAMILY; UNKNOWN_1.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
DNA-binding; Transcription regulation.
any aa: 31866 MW; F1D146DD95aa0CE3 CRC64;
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                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
          DB 2;
                    1.6e-37
        40.4%; Score 590.5;
llarity 44.5%; Pred. No. 1.6e
Conservative 51; Mismatches
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Best Local Similarity 39.3
Matches 125; Conservative
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InterPro; IPR001993;
                   Similarity
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Best Local (
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                                                                                                                                                                                                                                                                        69 HVQQVRLLEGDLQRWVPNLDEGGAPERLRIALNADSLATWWAAAVGDFCAERRVLLDLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDG--KLD
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PRINTS; PR00039; HTHLXSR.
PROSITE; PS00044; HTHLXSR_FAMILY; UNKNOWN_1.
SEQUENCE 300 AA; 32451 MW; BFC7F298E51CFBE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Created)
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01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
INHIBITOR OF CHROMOSOME INITIATION ICIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL: AE004852; AAG07751.1;
Interpro; IPR000847; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 RSLARLTDAVVDAAIEGL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 36.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=287;
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5.

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Local Similarity 28.09
Les 78; Conservative
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Best Local S
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Q91444
Q91444
D10 Q9
AC Q9
DT Q11D Q9
DT Q11D Q9
COS B8
CO
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                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAINEL TOR NIG661 / SEROTYPE 01;
MEDLINE-EL TOR NIG661 / SEROTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E. K., Peterson J.D., Unayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AARKMVLLQAETKAQLSGR - - LAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRLE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 DEAHTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGKLDWAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLVQ 65
                                                                                                                                                     Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M--PVLRFGPKDVLQDRDL------DGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 406:477-483(2000).
-!- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS
EMBL; AE004134; AAF93655.1; -.
TIGR; VC0482; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0039; HTHLYSR.
PROSTITE; PS00044; HTHLLYSR.FAMILY; UNKNOWN_1.
DNA-binding; Transcription regulation.
SEQUENCE 298 AA; 33653 MW; C7776C56A9FD2521 CRC64;
                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PROBABLE TRANSCRIPTIONAL REGULATOR.
PA3995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.8%; Score 361.5; DB 2; 29.9%; Pred. No. 5.1e-20; ative 65; Mismatches 116;
298 AA
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                                             Created)
  PRT;
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                                                                                                           CHROMOSOME INITIATION INHIBITOR
                                       01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cholerae.
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74 LYAYARNIVELEREARARLHGTPIRDRLRIGASEDFASAWLPRVLORFRRWHPEASIELK 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 PEPCVYREAAIT--ALGAAARPW-----RLVFESASMAGCLSAALAGFAVTVVARSQ--- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 IQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAGEV 62
STRAIN-PAO:
MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAOI, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 -GGATLTLRLEDEAHT----LSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 -TPSL-RDAYMVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119; Indels
                                                                                                                                                                                                                                                                            opportunistic pathogen.";
Nature 406.959-964(2000).
Nature 406.959-964(2000).
InterPro: IPR000847; -.
Pfam: PF00126; HTH_11: 1.
PROSTE: PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
SEQUENCE: 297 AA; 32515 WW; 3809B555D453B720 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 16, Last sequence update) (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| | | | : | | 34 -- MREGLRELGPEGGFPTLPEARFYAFSRQPSLAADALI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 EAIRRGL-----GWGLLPETQ-----AAPMLKAGEVI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.1%; Score 177; DB 2; 28.0%; Pred. No. 6.7e-06; tive 38; Mismatches 119;
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last ann
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LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAKATEAGEVLV 64
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                                                                                                                     12;
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                                                                                                                                                                                                                                                114 GGATLTLRLEDEAHTLSLLRRGDVLGAVTREAN---PVAGCEVVELGTMRHLAIATPSLR 170
                                                                                                                                                                                                                                                                        137 MSRDLSASYDRGELDLVLLKQ----RRASREALACWPEKTCWV-------DSAR 179
                                                                                                                                                                                                                                                                                                  DAYMVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRR-RVSIVPSA-EGFGEAIRR 228
                                                                                                                                                                                                                                                                                                                                                    229 GLGWGL-------LPETQAAPMLKAGEVILLDEIPIDTPMYWQRWRLESRSLARL 276
                                                                                                                                                                                             65 QAARKMVLLQAETKAQLSGRLAEIPLTIAINAD-----SLSTWFPPVFNEVASW 113
                                                                                                                                                                                                                                                                                                                                                                     6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAGEVLV 64
                                                                                                                     54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                        Length 300;
                                                                                       12.0%; Score 175; DB 2; Length 30 27.2%; Pred. No. 9.6e-06; Live 44; Mismatches 121; Indels
          Pfam; PF00126; HTH_1; 1.
PRINTS; PR00039; HTHLYSR.
PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
SEQUENCE 300 AA; 32670 MW; A56BD8C9BD07B67B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTH_LYSR_FAMILY; UNKNOWN_1.
; 31890 MW; 8F46BFB7356EA0AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PROBABLE TRANSCRIPTIONAL REGULATOR.
PA2758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=PAO1;
MEDLINE=20437337; PubMed=10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         opportunistic pathogen.";
Nature 406:595-964(2000).
EMBL; AE004703; AAG06146.1; -.
InterPro; IPR000847; -.
                                                                                        Query Match 12.0°
Best Local Similarity 27.2°
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa
 IPR001066;
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PROSITE; PS00044; HT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas
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InterPro;
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Gaps

16;

Length 295;

11.9%; Score 174; DB 2; Length 29 25.3%; Pred. No. 1.1e-05; tive 48; Mismatches 112; Indels

80; Conservative

Best Local Similarity Matches 80; Conserva

Query Match

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12;
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MEDLINE-2043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Rowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                              NEVASWGGATLTLRLEDEAHTLSLLRRGDV---LGAVTREANP-----VAGCEVVELGT 158
                                                                                                                                                                                                                       159 MRHLAIATPSLRDAYMVDGKLDWAAMPVLRFGPKDVLQDRD-LDGRVDGPVGRRRVSIVP 217
                                                                                                                                                                                                                                                                                                                                                           174 PRHPALOKPG-QALYL-------EELVNVRQILVASCDLPLADTRPLIAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                    S---AEGFG---EAIRRGLGWGLLPETQAAPMLKAGEVILLD-----EIPIDTPMYWQR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 ACWRTDSLGTALEMVEAGIGWGNFPLSRVAPLLATGRLVRLDFRNTKNELKLPVHAIW-- 273
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5 QLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPAKATEAGEVLV 64
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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SEQUENCE 310 AA; 34611 MW; 258E15C239BEFE7C CRC64;
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Last annotation update)
                                                                             QAARKMVLLQAETKAQLSGRLAEIP-----LTIAINAD----
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Nature 406:959-964(2000).
EMBL; AE004639; AAG05511.1;
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Best Local Similarity
Matches 77; Conserv
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Q91122;
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Figure 7. State 1. State 1. Mizoguchi S.D., Warrener P., Stover C.K., Pham X.D.T., Elwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Salar M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen."; Pseudomonas aeruginosa PA01, an Nature 406:999-964(2000).

InterPro, IPR000847;
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MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener
                                                                                                                                                                 Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
SEQUENCE 304 Aa; 33974 MW; 9AAZE242AE5CABBI CRC64;
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                                 Last sequence update)
Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PROBABLE TRANSCRIPTIONAL REGULATOR.
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                                                                                              PROBABLE TRANSCRIPTIONAL REGULATOR.
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MEDLINE=20437337; PubMed=10984043;
01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
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Best Local Similarity 26.73
Matches 76; Conservative
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Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Rowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.";
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                                                                                                                                                              204 VDGPVGRRRVSI----VPSAEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILLDEIPIDTP
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                                 ELGTMRHLAIATPSLRDAYMVDGKLDWAAMPVLRFGPKD-----VLQDRDLDGR--
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PROSITE; PS00044; HTHLYSR_FAMILY; UNKNOWN 1.
SEQUENCE 286 AA; 31641 MW; 36CDEB15C4F56947 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 IRRGLGWGLL------PETQAAPML 244
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROBABLE TRANSCRIPTIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE004560; AAĞ04698.1; -.
InterPro; IPR000847; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 27.78
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00126; HTH_1; 1.
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Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                     091435
091435;
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Q914D7;
                                                                                              159
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16;

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Length 304;

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Q914D7

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EMBL; AE004388; AAF96477.1;
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Q9KNH9
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STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; Comportunistic pathogen. Feedunce of Pseudomonas aeruginosa PAO1, an Nature 406:959-964(2000).

BMBL, AEONGAT7, AAGOS885.1; --
InterPro: IPR001066; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVQAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTLRL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDEA----HTLSLLRRGDVLGAVTREANPVAGCEVVELGTMRHLAIATPSLRDAYMVDGK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 LLGYARRLLRLSDEASEALSPAHGDGVLRLGVPEDLAGEVLMPVLTRFTE---ERPRLRL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 IQLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQ-PAKATEAGEV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 LASLVAAVGAGLGVSLLPLGCVGPEHRLLGAQAGFPPIAGLELALYARPELDS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDW---AAMPVLRFGPKDVLQDRDLDGRVDGPVGR-RRVSIVPSAEGFGE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AIRRGLGWGLLP------ETQAA-PMLKAGEVILLDEIPIDTPMYWQRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVESGLSHHLLRLYRSGELDLLLVKQWGADSDC------HARWAEP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                    Interio, itanocatorio, peam; propilo p
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    10.4%; Score 152.5; DB 2; 25.9%; Pred. No. 0.00049; Live 41; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSCRIPTIONAL REGULATOR, LYSR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:| || | : || :||:
--AGRTLRDRLRD-LCDARLEGLQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 RLESRSLA-RLTDAVVDAAIEGLR 289
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 25.9%
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 406:477-483(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
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SEQUENCE FROM N.A.
STRAIR=L TOR NIÉ961 / SEROTYPE 01;
MEDLINE=L TOR NIÉ961 / SEROTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Raad T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                              56 ATEAGEVLVQAARKMVLLQAETK----AQLSGRLAEIPLTIAINADSLSTWFPP---VFN 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVASWGGATLT-LRLEDE--AHTLSLLR--RGDVLGAVTREANPVAGCEVVELGTMRHLA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 IATPS------LRDAY----MVDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 PVGRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILL---DEIPIDTPMYW 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                    1 MNPIQLDTLLSIID----EGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRT-QPAK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 VAAPTHYVHRRSGEFNEEAREKYRAIAIADTAREQPAMSV-----NILQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHOLEIGE. ,
Nature 406:477-483(2000).
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                                                                                                                                                                                                                                                67;
                                                                                                                                                                                             Length 295;
TIGR; VCAO575; -.
InterPro; IPR000847; -.
Pfam; PF00126; HTH_1; 1.
PROSITE: PS00044; HTH_1YSR_FAMILY; UNKNOWN_1.
PROSITE: PS00044; HTH_1YSR_FAMILY; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00126; HTH_1; 1.
PRINTS: PR00039; HTHLYSR.
DNA-binding; Transcription regulation.
SEQUENCE 302 AA; 34281 MW; DEEEB28511225CE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
OL-OCT-2000 (TrEMBLrel. 15, Last sequence update)
OL-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRANSCRIPTIONAL REGULATOR, LYSR FAMILY.
                                                                                                                                                                                       Score 152.5; DB 2;
Pred. No. 0.0005;
2; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 AA
                                                                                                                                                                                                                                             62;
                                                                                                                                                                                             10.4%;
25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO THE LYSR EMBL; AE004342; AAF95899.1; TIGR; VC2760; -.
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 QRWRL-ESRS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| :: |::|
273 RRNQMGEAKS 282
                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio cholerae.
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67 LEHARRLV-----SGAHNLANEIALFNGLEAGELRFGAGPAPATWLVPRAVGRFN 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 DLDGRVD-GPV----GRRRVSIVPSAEGFGEAIRRGLGWGLLPETQAAPMLKAG-EVIL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20437337; PubMed-10984043; Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Golter D.Y., Tolentino E., Wastbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PADI, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 QLDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAGEVL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 REANPVAGCEVVELGTMRHLAIAT----PSLRDAYMVDGKLDWAAMPVLRFGPKDVLQDR
                        ----LDWAAMP----VLRFGPKDVLQDRDLDGRVDGPVGRRVSIV
                                                                     198 YLREHGVPASPGELPEHAGIDWDNLSPPYAWRF*****QHDGKLQHLRPKRARLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 VQAARKMVLLQAETKAQLSG--RLA-EIPLTIAINADSL-----STWFPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 VRYPKARVSFQVEHWQALNRRLQAEEFEFFVADTRHFEADPQYRTSRLRPRRWHF --- CC
                                                                                                                    PSAEGFGEAIRRGLGWGLLPETQAAPMLKAGEVILL---DEIPIDTP--MYWQRWRLESR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.2%; Score 149; DB 2; Length 303;
24.9%; Pred. No. 0.00095;
Live 47; Mismatches 102; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00126; HTH_1; 1.
PRINTS; PR00039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR.FAMILY; UNKNOWN_1.
PROSINCE 303 AA; 33686 MW; FCE1C76FD4F47874 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 LDEIPIDTPMYWQRWRLESR---SLARLTDAVVD 282
                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created 01-MAR-2001 (TrEMBLrel. 16, Last se 01-MAR-2001 (TrEMBLrel. 16, Last an probable TRANSCRIPTIONAL REGULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         opportunistic pathogen.";
Nature 406:959-964(2000),
EMBL; AE004659; AAG05722.1;
InterPro; IPR000847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa
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Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                        169 LRDAYMVDGK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=287;
                                                                                                                                                                                                               272 SLARL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas
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Q911E4
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                                                                                                                                                                                                                                        68 LEARQLLRQMEEIRAQTKRAAHGWRKTLKVTLD-NVVKLDKMKPMVEAFYQTFDFAELQI 126
                                                                                                                                                                                                                                                                                  121 RLEDEAHTLSLLRRGD---VLGAVTREANPVAG-CEVVELGTMRHLAIATPS---LRDAY 173
                                                                                                                                                                                                                                                                                                                174 MYDGKLDWAAMPVLRFGPKDVLQDRDLDGRVDGPVGRRRVSIVPSAEGFGEAIRRGLGWG 233
                                                                                                                                                                                                                                                                                                                                                                                                           Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAOI, an
                                                                                                                                                                                         65 ----QAARKMVLLQAETKAQLSGRLAEIPLTIAINADSLSTWFPPVFNEVASWGGATLTL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 AGEVLVQAARKMV----LLQAETKAQLSG--RLAEIPLTIAINADSLSTWFPPVFNEVAS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 WGGATLTLRLEDEAHTLSLLRRGDVLGAV--TREANPVAGCEVV--ELGTMRHLAIATPS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 NPGLDVQLRLIGSFIDL----QGEHLGEVDLVLRAGPLPDSRLVATSLAPMVRVVCASPE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 AGLAFADRARRIVTELRLARAEAVSLSTAPQGLIRIDAPVPFGRRHLA---PAVADFLKA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 DTL-----LSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSRTQPA-KATE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 DILSEQFVLYLDVLDGGSFSAAARKHPLTPSAVARRMDALERAVGSTLLVRTTHAVRATP 84
                                                                                              6 LDTLLSIIDEGSFEGASLALSISPSAVSQRVKALEHHVGRVLVSR-TQPAKATEAGEVLV 64
                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 339;
Length 302;
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PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
SEQUENCE 339 AA; 37280 MW; BDFB5DE083D2F86D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
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10.3%; Score 151; DB 2; L 26.1%; Pred. No. 0.00067; Live 53; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.2%; Score 149.5; DB 2; 27.2%; Pred. No. 0.001; live 40; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created 01-MAR-2001 (TrEMBLrel. 16, Last se 01-MAR-2001 (TrEMBLrel. 16, Last an PROBABLE TRANSCRIPTIONAL REGULATOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 YMPRHMAQPLLASGQLVEKVLPDE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 LLPETQAAPMLKAG---EVILLDE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 406:959-964(2000).
EMBL; AE004711; AAG06236.1; -.
InterPro; IPR000847; -.
                                                 Conservative
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                           Local Similarity
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NCBI_TaxID=287;
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